



SUBSTITUTE SEQUENCE LISTING

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TECH CENTER 1600/2900

(1) GENERAL INFORMATION:

(i) APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

(ii) TITLE OF INVENTION: Telomerase Reverse Transcriptase

(iii) NUMBER OF SEQUENCES: 477

(iv) CORRESPONDENCE ADDRESS:

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(D) STATE: California
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(F) ZIP: 94111-3834

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/974,584
(B) FILING DATE: 19-NOV-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/724,643
(B) FILING DATE: 01-OCT-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/844,419
(B) FILING DATE: 18-APR-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/846,017
(B) FILING DATE: 25-APR-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/851,843
(B) FILING DATE: 06-MAY-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/854,050
(B) FILING DATE: 09-MAY-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/911,312
(B) FILING DATE: 14-AUG-1997

- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 08/912,951
 (B) FILING DATE: 14-AUG-1997
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 08/915,503
 (B) FILING DATE: 14-AUG-1997
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: WO PCT/US97/17618
 (B) FILING DATE: 01-OCT-1997
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: WO PCT/US97/17885
 (B) FILING DATE: 01-OCT-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Einhorn, Gregory P.
 (B) REGISTRATION NUMBER: 38,440
 (C) REFERENCE/DOCKET NUMBER: 015389-002950US
- (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: (415) 576-0200
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 101..3196
 (D) OTHER INFORMATION: /codon= (seq: "tga", aa: Cys)
 /note= "Euplotes aediculatus 123 kD
 telomerase subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT AACCTCAGTA	60
TTAATAAGCT CAGATTTTAA ATATTAATTA CAAACCTAA ATG GAG GTT GAT GTT	115
Met Glu Val Asp Val	
1 5	
GAT AAT CAA GCT GAT AAT CAT GGC ATT CAC TCA GCT CTT AAG ACT TGT	163
Asp Asn Gln Ala Asp Asn His Gly Ile His Ser Ala Leu Lys Thr Cys	
10 15 20	
GAA GAA ATT AAA GAA GCT AAA ACG TTG TAC TCT TGG ATC CAG AAA GTT	211
Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser Trp Ile Gln Lys Val	
25 30 35	

ATT AGA TGA AGA AAT CAA TCT CAA AGT CAT TAT AAA GAT TTA GAA GAT Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr Lys Asp Leu Glu Asp 40 45 50	259
ATT AAA ATA TTT GCG CAG ACA AAT ATT GTT GCT ACT CCA CGA GAC TAT Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala Thr Pro Arg Asp Tyr 55 60 65	307
AAT GAA GAA GAT TTT AAA GTT ATT GCA AGA AAA GAA GTA TTT TCA ACT Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys Glu Val Phe Ser Thr 70 75 80 85	355
GGA CTA ATG ATC GAA CTT ATT GAC AAA TGC TTA GTT GAA CTT CTT TCA Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu Val Glu Leu Leu Ser 90 95 100	403
TCA AGC GAT GTT TCA GAT AGA CAA AAA CTT CAA TGA TTT GGA TTT CAA Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln Cys Phe Gly Phe Gln 105 110 115	451
CTT AAG GGA AAT CAA TTA GCA AAG ACC CAT TTA TTA ACA GCT CTT TCA Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu Leu Thr Ala Leu Ser 120 125 130	499
ACT CAA AAG CAG TAT TTC TTT CAA GAC GAA TGG AAC CAA GTT AGA GCA Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp Asn Gln Val Arg Ala 135 140 145	547
ATG ATT GGA AAT GAG CTC TTC CGA CAT CTC TAC ACT AAA TAT TTA ATA Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr Thr Lys Tyr Leu Ile 150 155 160 165	595
TTC CAG CGA ACT TCT GAA GGA ACT CTT GTT CAA TTT TGC GGG AAT AAC Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln Phe Cys Gly Asn Asn 170 175 180	643
GTT TTT GAT CAT TTG AAA GTC AAC GAT AAG TTT GAC AAA AAG CAA AAA Val Phe Asp His Leu Lys Val Asn Asp Lys Phe Asp Lys Lys Gln Lys 185 190 195	691
GGT GGA GCA GCA GAC ATG AAT GAA CCT CGA TGT TGA TCA ACC TGC AAA Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys Ser Thr Cys Lys 200 205 210	739
TAC AAT GTC AAG AAT GAG AAA GAT CAC TTT CTC AAC AAC ATC AAC GTG Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn Asn Ile Asn Val 215 220 225	787
CCG AAT TGG AAT AAT ATG AAA TCA AGA ACC AGA ATA TTT TAT TGC ACT Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg Ile Phe Tyr Cys Thr 230 235 240 245	835
CAT TTT AAT AGA AAT AAC CAA TTC TTC AAA AAG CAT GAG TTT GTG AGT His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys His Glu Phe Val Ser 250 255 260	883
AAC AAA AAC AAT ATT TCA GCG ATG GAC AGA GCT CAG ACG ATA TTC ACG Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala Gln Thr Ile Phe Thr 265 270 275	931

AAT ATA TTC AGA TTT AAT AGA ATT AGA AAG AAG CTA AAA GAT AAG GTT Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys Leu Lys Asp Lys Val 280 285 290	979
ATC GAA AAA ATT GCC TAC ATG CTT GAG AAA GTC AAA GAT TTT AAC TTC Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val Lys Asp Phe Asn Phe 295 300 305	1027
AAC TAC TAT TTA ACA AAA TCT TGT CCT CTT CCA GAA AAT TGG CGG GAA Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro Glu Asn Trp Arg Glu 310 315 320 325	1075
CGG AAA CAA AAA ATC GAA AAC TTG ATA AAT AAA ACT AGA GAA GAA AAG Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys Thr Arg Glu Glu Lys 330 335 340	1123
TCG AAG TAC TAT GAA GAG CTG TTT AGC TAC ACA ACT GAT AAT AAA TGC Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr Thr Asp Asn Lys Cys 345 350 355	1171
GTC ACA CAA TTT ATT AAT GAA TTT TTC TAC AAT ATA CTC CCC AAA GAC Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn Ile Leu Pro Lys Asp 360 365 370	1219
TTT TTG ACT GGA AGA AAC CGT AAG AAT TTT CAA AAG AAA GTT AAG AAA Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln Lys Lys Val Lys Lys 375 380 385	1267
TAT GTG GAA CTA AAC AAG CAT GAA CTC ATT CAC AAA AAC TTA TTG CTT Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys Asn Leu Leu Leu 390 395 400 405	1315
GAG AAG ATC AAT ACA AGA GAA ATA TCA TGG ATG CAG GTT GAG ACC TCT Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln Val Glu Thr Ser 410 415 420	1363
GCA AAG CAT TTT TAT TAT TTT GAT CAC GAA AAC ATC TAC GTC TTA TGG Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile Tyr Val Leu Trp 425 430 435	1411
AAA TTG CTC CGA TGG ATA TTC GAG GAT CTC GTC GTC TCG CTG ATT AGA Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg 440 445 450	1459
TGA TTT TTC TAT GTC ACC GAG CAA CAG AAA AGT TAC TCC AAA ACC TAT Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr 455 460 465	1507
TAC TAC AGA AAG AAT ATT TGG GAC GTC ATT ATG AAA ATG TCA ATC GCA Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala 470 475 480 485	1555
GAC TTA AAG AAG GAA ACG CTT GCT GAG GTC CAA GAA AAA GAG GTT GAA Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu 490 495 500	1603
GAA TGG AAA AAG TCG CTT GGA TTT GCA CCT GGA AAA CTC AGA CTA ATA Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile 505 510 515	1651

CCG AAG AAA ACT ACT TTC CGT CCA ATT ATG ACT TTC AAT AAG AAG ATT Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile 520 525 530	1699
GTA AAT TCA GAC CGG AAG ACT ACA AAA TTA ACT ACA AAT ACG AAG TTA Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu 535 540 545	1747
TTG AAC TCT CAC TTA ATG CTT AAG ACA TTG AAG AAT AGA ATG TTT AAA Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys 550 555 560 565	1795
GAT CCT TTT GGA TTC GCT GTT TTT AAC TAT GAT GAT GTA ATG AAA AAG Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys 570 575 580	1843
TAT GAG GAG TTT GTT TGC AAA TGG AAG CAA GTT GGA CAA CCA AAA CTC Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu 585 590 595	1891
TTC TTT GCA ACT ATG GAT ATC GAA AAG TGA TAT GAT AGT GTA AAC AGA Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val Asn Arg 600 605 610	1939
GAA AAA CTA TCA ACA TTC CTA AAA ACT ACT AAA TTA CTT TCT TCA GAT Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser Ser Asp 615 620 625	1987
TTC TGG ATT ATG ACT GCA CAA ATT CTA AAG AGA AAG AAT AAC ATA GTT Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys Asn Asn Ile Val 630 635 640 645	2035
ATC GAT TCG AAA AAC TTT AGA AAG AAA GAA ATG AAA GAT TAT TTT AGA Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys Asp Tyr Phe Arg 650 655 660	2083
CAG AAA TTC CAG AAG ATT GCA CTT GAA GGA GGA CAA TAT CCA ACC TTA Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln Tyr Pro Thr Leu 665 670 675	2131
TTC AGT GTT CTT GAA AAT GAA CAA AAT GAC TTA AAT GCA AAG AAA ACA Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn Ala Lys Lys Thr 680 685 690	2179
TTA ATT GTT GAA GCA AAG CAA AGA AAT TAT TTT AAG AAA GAT AAC TTA Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys Lys Asp Asn Leu 695 700 705	2227
CTT CAA CCA GTC ATT AAT ATT TGC CAA TAT AAT TAC ATT AAC TTT AAT Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr Ile Asn Phe Asn 710 715 720 725	2275
GGG AAG TTT TAT AAA CAA ACA AAA GGA ATT CCT CAA GGT CTT TGA GTT Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val 730 735 740	2323
TCA TCA ATT TTG TCA TCA TTT TAT TAT GCA ACA TTA GAG GAA AGC TCC Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser 745 750 755	2371

TTA GGA TTC CTT AGA GAT GAA TCA ATG AAC CCT GAA AAT CCA AAT GTT Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn Pro Asn Val 760 765 770	2419
AAT CTT CTA ATG AGA CTT ACA GAT GAC TAT CTT TTG ATT ACA ACT CAA Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln 775 780 785	2467
GAG AAT AAT GCA GTA TTG TTT ATT GAG AAA CTT ATA AAC GTA AGT CGT Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg 790 795 800 805	2515
GAA AAT GGA TTT AAA TTC AAT ATG AAG AAA CTA CAG ACT AGT TTT CCA Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser Phe Pro 810 815 820	2563
TTA AGT CCA AGC AAA TTT GCA AAA TAC GGA ATG GAT AGT GTT GAG GAG Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp Ser Val Glu Glu 825 830 835	2611
CAA AAT ATT GTT CAA GAT TAC TGC GAT TGG ATT GGC ATC TCA ATT GAT Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly Ile Ser Ile Asp 840 845 850	2659
ATG AAA ACT CTT GCT TTA ATG CCA AAT ATT AAC TTG AGA ATA GAA GGA Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu Arg Ile Glu Gly 855 860 865	2707
ATT CTG TGT ACA CTC AAT CTA AAC ATG CAA ACA AAG AAA GCA TCA ATG Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys Lys Ala Ser Met 870 875 880 885	2755
TGG CTC AAG AAG AAA CTA AAG TCG TTT TTA ATG AAT AAC ATT ACC CAT Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn Asn Ile Thr His 890 895 900	2803
TAT TTT AGA AAG ACG ATT ACA ACC GAA GAC TTT GCG AAT AAA ACT CTC Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala Asn Lys Thr Leu 905 910 915	2851
AAC AAG TTA TTT ATA TCA GGC GGT TAC AAA TAC ATG CAA TGA GCC AAA Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met Gln Cys Ala Lys 920 925 930	2899
GAA TAC AAG GAC CAC TTT AAG AAG AAC TTA GCT ATG AGC AGT ATG ATC Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met Ser Ser Met Ile 935 940 945	2947
GAC TTA GAG GTA TCT AAA ATT ATA TAC TCT GTA ACC AGA GCA TTC TTT Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr Arg Ala Phe Phe 950 955 960 965	2995
AAA TAC CTT GTG TGC AAT ATT AAG GAT ACA ATT TTT GGA GAG GAG CAT Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe Gly Glu Glu His 970 975 980	3043
TAT CCA GAC TTT TTC CTT AGC ACA CTG AAG CAC TTT ATT GAA ATA TTC Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe Ile Glu Ile Phe 985 990 995	3091

AGC ACA AAA AAG TAC ATT TTC AAC AGA GTT TGC ATG ATC CTC AAG GCA 3139
 Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys Met Ile Leu Lys Ala
 1000 1005 1010

AAA GAA GCA AAG CTA AAA AGT GAC CAA TGT CAA TCT CTA ATT CAA TAT 3187
 Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln Ser Leu Ile Gln Tyr
 1015 1020 1025

GAT GCA TAGTCGACTA TTCTAACTTA TTTTGGAAG TTAATTTTCA ATTTTGTCT 3243
 Asp Ala
 1030

TATATACTGG GGTTTTGGGG TTTTGGGGTT TTGGGG 3279

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
 1 5 10 15
 Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
 20 25 30
 Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
 35 40 45
 Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
 50 55 60
 Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys
 65 70 75 80
 Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu
 85 90 95
 Val Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln
 100 105 110
 Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu
 115 120 125
 Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp
 130 135 140
 Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr
 145 150 155 160
 Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln
 165 170 175
 Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe
 180 185 190

Asp Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys
 195 200 205
 Cys Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu
 210 215 220
 Asn Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg
 225 230 235 240
 Ile Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys
 245 250 255
 His Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala
 260 265 270
 Gln Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys
 275 280 285
 Leu Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val
 290 295 300
 Lys Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro
 305 310 315 320
 Glu Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys
 325 330 335
 Thr Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr
 340 345 350
 Thr Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn
 355 360 365
 Ile Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln
 370 375 380
 Lys Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His
 385 390 395 400
 Lys Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met
 405 410 415
 Gln Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn
 420 425 430
 Ile Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val
 435 440 445
 Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser
 450 455 460
 Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met
 465 470 475 480
 Lys Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln
 485 490 495
 Glu Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly
 500 505 510

Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr
 515 520 525
 Phe Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr
 530 535 540
 Thr Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys
 545 550 555 560
 Asn Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp
 565 570 575
 Asp Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val
 580 585 590
 Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
 595 600 605
 Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
 610 615 620
 Leu Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg
 625 630 635 640
 Lys Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met
 645 650 655
 Lys Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly
 660 665 670
 Gln Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu
 675 680 685
 Asn Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe
 690 695 700
 Lys Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn
 705 710 715 720
 Tyr Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro
 725 730 735
 Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr
 740 745 750
 Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro
 755 760 765
 Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu
 770 775 780
 Leu Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu
 785 790 795 800
 Ile Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu
 805 810 815
 Gln Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met
 820 825 830

Asp Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile
 835 840 845
 Gly Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn
 850 855 860
 Leu Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr
 865 870 875 880
 Lys Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met
 885 890 895
 Asn Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe
 900 905 910
 Ala Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr
 915 920 925
 Met Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala
 930 935 940
 Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val
 945 950 955 960
 Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile
 965 970 975
 Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His
 980 985 990
 Phe Ile Glu Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys
 995 1000 1005
 Met Ile Leu Lys Ala Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln
 1010 1015 1020
 Ser Leu Ile Gln Tyr Asp Ala
 1025 1030

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1762
- (D) OTHER INFORMATION: /note= "DNA encoding three open reading frames (ORF) for Euplotes aediculatus 43 kD telomerase protein subunit given in SEQ ID NOS:4-6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCCAAAACC CCAAAACCCC AAAACCCCTA TAAAAAAGA AAAAAATTGAG GTAGTTTAGA	60
AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA TTTGGATGAT ATAGAAAATT	120
TACTTCCTAA TACATTCAAC AAGTATAGCA GCTCTTGTAG TGACAAGAAA GGATGCAAAA	180
CATTGAAATC TGGCTCGAAA TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG	240
AGTTCTACTT CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA	300
AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA AATCAGGTAA	360
TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA TTATGGAGAA AATTACTTAA	420
TACTAAAAGG TAAACAGTTT GGATTATTTT CCTAGCCAAC AATGATGAGT ATATTAAATT	480
CATATGAGAA TGAGTCAAAG GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT	540
AAAACGCAAG AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCG	600
TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC TTGAGACAAT	660
TGAAAAAGCT GTTTACAAC GAAGGAATCG CAGTTCTGAA AGTTCTGATG TGTATGCCAT	720
TATTTTGTGA ATTAATCTCA AATATCTTAT CTCAATTTAA TGGATAGCTA TAGAAACAAA	780
CCAAATAAAC CATGCAAGTT TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC	840
TGAATTTATA TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC	900
TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT AAAAGAAGCA	960
GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT TTGTTGATTC TTCTGTAACC	1020
GGAATTAACA ACAAGAATAT TAGCAACGAA AAAGAAGAAG AGCTATCACA ATCCTGATTC	1080
TTAAAGATTT CAAAAATTCC AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG	1140
TTTTTCATTT CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA	1200
GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT TCACATTCAT	1260
AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA GCAGTCATCC GTTTTAAAAA	1320
TAGTGCTATG AGGACTAAAT TTTTAGAGTC AAGAAATGGA GCCGAAATCT TAATCAAAAA	1380
GAATTGCGTC GATATTGCAA AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA	1440
ATCTTGATTG ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATT AAGAAATAAA	1500
GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG CGATCTTCAA	1560
TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA ATACAAACCT TGGTCAAAAT	1620
ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA AAAGAAAAA TAAGGCAATA AATAAAATGA	1680
GTACAGAAGT GAAGAAATAA AAGATTTATT TTTTCAATA ATTTATTGAA AAGAGGGGTT	1740
TTGGGGTTTT GGGGTTTTGG GG	1762

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..300
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 1-300 may be
present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 630
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at position 630 may be
present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 649..663
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 649-663 may be
present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 674..688
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 674-688 may be
present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 701..706
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 701-706 may be
present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 771..790
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 771-790 may be
present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 887..937
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 887-937 may be
present or absent"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 965..994

(D) OTHER INFORMATION: /product= "OTHER"

/note= "Xaa at positions 965-994 may be present or absent"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1018..1027

(D) OTHER INFORMATION: /product= "OTHER"

/note= "Xaa at positions 1018-1027 may be present or absent"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	1	5	10	15
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	20	25	30	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	35	40	45	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	50	55	60	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	65	70	75	80
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	85	90	95	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	100	105	110	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	115	120	125	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	130	135	140	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	145	150	155	160
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	165	170	175	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	180	185	190	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	195	200	205	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	210	215	220	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
225					230					235					240
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				245					250					255	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			260					265					270		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		275					280					285			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	290					295					300				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
305					310					315					320
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				325					330					335	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			340					345					350		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		355					360					365			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	370					375					380				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
385					390					395					400
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				405					410					415	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			420					425					430		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		435					440					445			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	450					455					460				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
465					470					475					480
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				485					490					495	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			500					505					510		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		515					520					525			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	530					535					540				

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
545					550					555						560
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				565					570						575	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			580					585						590		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		595					600					605				
Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Phe	Tyr	Xaa	Thr	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
610						615					620					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Xaa	Xaa	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
625					630					635						640
Xaa	Xaa	Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			645						650						655	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Val	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			660					665						670		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		675						680					685			
Xaa	Xaa	Xaa	Arg	Xaa	Xaa	Pro	Lys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
690					695						700					
Xaa	Xaa	Arg	Xaa	Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
705					710					715						720
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				725					730						735	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			740					745						750		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		755					760					765				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
770						775					780					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Asp	Xaa	Xaa
785					790					795					800	
Xaa	Xaa	Xaa	Tyr	Asp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				805					810					815		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			820					825						830		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		835					840					845				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
850						855					860					

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 865 870 875 880
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 885 890 895
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 900 905 910
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 915 920 925
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Gly Xaa
 930 935 940
 Xaa Gln Gly Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 945 950 955 960
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 965 970 975
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 980 985 990
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Asp Xaa Leu Xaa Xaa Xaa Xaa
 995 1000 1005
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1010 1015 1020
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys
 1025 1030 1035 1040

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCCGGATCC TGCGCATGTG TGAGCCGAGT CCTGGG

36

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Val Asp Asp Phe Leu
1 5

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Trp Xaa Gly Xaa Ser Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Xaa Leu Gly Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 83 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Asp Ile Asp Leu Asp Asp Ile Glu Asn Leu Leu Pro Asn Thr Phe Asn
1           5           10           15
Lys Tyr Ser Ser Ser Cys Ser Asp Lys Lys Gly Cys Lys Thr Leu Lys
          20           25           30
Ser Gly Ser Lys Ser Pro Ser Leu Thr Ile Pro Lys Leu Gln Lys Gln
          35           40           45
Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn Asp Ser Phe Leu
          50           55           60
Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val Glu Ile Glu Thr
65           70           75           80
Leu Leu Met

```

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Asn Val Lys Ser Ala Lys Ile Glu Ser Ser Ser Leu Glu Ser Leu Glu
1           5           10           15
Asp Ile Asp Ser Leu Cys Lys Ser Ile Ala Ser Cys Lys Asn Leu Gln
          20           25           30
Asn Val Asn Ile Ile Ala Ser Leu Leu Tyr Pro Asn Asn Ile Gln Lys
          35           40           45
Asn Pro Phe Asn Lys Pro Asn Leu Leu Phe Phe Lys Gln Phe Glu Gln
          50           55           60
Leu Lys Asn Leu Glu Asn Val Ser Ile Asn Cys Ile Leu Asp Gln His
65           70           75           80
Ile Leu Asn Ser Ile Ser Glu Phe Leu Glu Lys Asn Lys Lys Ile Lys
          85           90           95
Ala Phe Ile Leu
          100

```

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Met Glu Met Asp Ile Asp Leu Asp Asp Ile Glu Asn Leu Leu Pro Asn
1           5           10           15

Thr Phe Asn Lys Tyr Ser Ser Ser Cys Ser Asp Lys Lys Gly Cys Lys
          20           25           30

Thr Leu Lys Ser Gly Ser Lys Ser Pro Ser Leu Thr Ile Pro Lys Leu
          35           40           45

Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn Asp
          50           55           60

Ser Phe Leu Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val Glu
65           70           75           80

Ile Glu Thr Leu Leu
          85

```

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Ile Glu Leu Ala Ile Lys Ile Ala Val Asn Lys Asn Leu Asp Glu Ile
1           5           10           15

Lys Gly His Thr Ala Ile Phe Ser Asp Val Ser Gly Ser Met Ser Thr
          20           25           30

Ser Met Ser Gly Gly Ala Lys Lys Tyr Gly Ser Val Arg Thr Cys Leu
          35           40           45

Glu Cys Ala Leu Val Leu Gly Leu Met Val Lys Gln Arg Cys Glu Lys
          50           55           60

Ser Ser Phe Tyr Ile Phe Ser Ser Pro Ser Ser Gln Cys Asn Lys Cys
65           70           75           80

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

Xaa Xaa Asp Asp Xaa
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Val"

(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Xaa Xaa Asp Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Xaa Xaa Asp Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 28
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 31
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Phe	Trp
1				5						10					15	
Xaa	Thr	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Xaa
			20						25					30		
Xaa Trp																

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 30
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Phe	Trp
1				5				10						15	
Xaa	Thr	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa
			20					25					30		
Xaa	Xaa	Trp													
		35													

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7..8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10..11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 25
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 28..29
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 31

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1 5 10 15

Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa
20 25 30

Xaa Trp

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7..8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10..11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 25
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29..30
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1           5           10           15

Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa
          20           25           30

Xaa Xaa Trp
          35

```

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Gly Ser Val Thr Lys
1           5

```

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Asn Ser Ala Val Asp
1 5

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTTCAAGACC ATCCTGGACT TTCGAAACGC GGCCGCCACC GCGGTGGAGC TCC

53

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Leu	Gln	Lys	Gln	Leu	Glu	Phe	Tyr	Phe	Ser	Asp	Ala	Asn	Leu	Tyr	Asn
1				5					10					15	
Asp	Ser	Phe	Leu	Arg	Lys	Leu	Val	Leu	Lys	Ser	Gly	Glu	Gln	Arg	Val
			20					25					30		
Glu	Ile	Glu	Thr	Leu	Leu	Met									
			35												

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Ile Cys His Gln Xaa Glu Tyr Tyr Phe Gly Asp Phe Asn Leu Pro Arg
1           5           10           15
Asp Lys Phe Leu Lys Glu Gln Ile Lys Leu Asp Glu Gly Trp Val Pro
                20           25           30
Leu Glu Ile Met Ile Lys
                35

```

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 38 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

Ile Cys Glu Gln Ile Glu Tyr Tyr Phe Gly Asp His Asn Leu Pro Arg
1           5           10           15
Asp Lys Phe Leu Lys Gln Gln Ile Leu Leu Asp Asp Gly Trp Val Pro
                20           25           30
Leu Glu Thr Met Ile Lys
                35

```

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Ile Leu Arg Gln Val Glu Tyr Tyr Phe Gly Asp Ala Asn Leu Asn Arg
1           5           10           15
Asp Lys Phe Leu Arg Glu Gln Ile Gly Lys Asn Glu Asp Gly Trp Val
                20           25           30
Pro Leu Ser Val Leu Val Thr
                35

```


(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Cys	Leu	Lys	Gln	Val	Glu	Phe	Tyr	Phe	Ser	Glu	Phe	Asn	Phe	Pro	Tyr
1				5					10					15	
Asp	Arg	Phe	Leu	Arg	Thr	Thr	Ala	Glu	Lys	Asn	Asp	Gly	Trp	Val	Pro
			20					25					30		
Ile	Ser	Thr	Ile	Ala	Thr										
			35												

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TAGACCTGTT AGTGTACATT TGAATTGAAG C

31

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TAGACCTGTT AGGTTGGATT TGTGGCATCA

30

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAAAACCCCA AAACCTAACA GGTCTA

26

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCGGGAATTC TAATACGACT CACTATAGGG AAGAACTCT GATGAGGCCG AAAGGCCGAA

60

ACTCCACGAA AGTGGAGTAA GTTTCTCGAT AATTGATCTG TAG

103

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGGGGATCCT CTTCAAAGA TGAGAGGACA GCAAAC

36

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCCCAAAACC CCAAACCCC AAAACCCCA CAGGGGTTTT GGGGTTTTGG GTTTTGGGG

60

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCAAAACCCC AAAACCCCAA AACCCCCACA GGGGTTTGGG GGTTTGGGG TTTTGGGG

58

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAAACCCCAA AACCCCAAAA CCCCCACAGG GGTTTGGGG TTTTGGGGTT TTGGGG

56

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AACCCCAAAA CCCCAAACC CCCACAGGGG TTTTGGGGTT TTGGGGTTTT GGGG

54

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CCCCAAAACC CCAAACCCC CACAGGGGTT TTGGGGTTTT GGGGTTTT

48

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAAACCCCAA AACCCCAAAA CCCCACAGG GGTTTTGGGG TTTTGGGGTT TT

52

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACCCCAAAA CCCCAAACC CCCACAGGG TTTTGGGGTT TTGGGGTTTT

50

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGGGAAGCTT TAATACGACT CACTATAGGG TTGCGGAGGG TGGGCCTG

48

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCAAAACCCC AAAACCCCCA CAGGGGTTTT GGGGTTTGG GGTTTT

46

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAAACCCCAA AACCCCCACA GGGGTTTTGG GGTTTTGGGG TTTT

44

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CAAAACCCCA AAACC

15

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTTTGGGG

8

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGGGTTTT

8

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Arg Phe Ile Pro Lys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TCTRAARTAR TGDGTNADRT TRTTCAT

27

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCGGATCCAT GAAYCCWGAR AAYCCWAAYG T

31

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

NNNGTNACHG GHATHAAYAA

20

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

DGCDGTYTCY TGRTCRTTTRT A

21

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2421 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 92..2251
- (D) OTHER INFORMATION: /codon= (seq: "taa", aa: Gln)
/codon= (seq: "tag", aa: Gln)
/note= "Tetrahymena thermophila 80 kD
TRT protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AACTCATTTA ATTACTAATT TAATCAACAA GATTGATAAA AAGCAGTAAA TAAAACCCAA

60

TAGATTTAAT TTAGAAAGTA TCAATTGAAA A ATG GAA ATT GAA AAC AAC TAA
Met Glu Ile Glu Asn Asn Gln

112

1

5

GCA CAA TAG CCA AAA GCC GAA AAA TTG TGG TGG GAA CTT GAA TTA GAG Ala Gln Gln Pro Lys Ala Glu Lys Leu Trp Trp Glu Leu Glu Leu Glu	160
10 15 20	
ATG CAA GAA AAC CAA AAT GAT ATA TAA GTT AGG GTT AAG ATT GAC GAT Met Gln Glu Asn Gln Asn Asp Ile Gln Val Arg Val Lys Ile Asp Asp	208
25 30 35	
CCT AAG CAA TAT CTC GTG AAC GTC ACT GCA GCA TGT TTG TTG TAG GAA Pro Lys Gln Tyr Leu Val Asn Val Thr Ala Ala Cys Leu Leu Gln Glu	256
40 45 50 55	
GGT AGT TAC TAC TAA GAT AAA GAT GAA AGA AGA TAT ATC ATC ACT AAA Gly Ser Tyr Tyr Gln Asp Lys Asp Glu Arg Arg Tyr Ile Ile Thr Lys	304
60 65 70	
GCA CTT CTT GAG GTG GCT GAG TCT GAT CCT GAG TTC ATC TGC TAG TTG Ala Leu Leu Glu Val Ala Glu Ser Asp Pro Glu Phe Ile Cys Gln Leu	352
75 80 85	
GCA GTC TAC ATC CGT AAT GAA CTT TAC ATC AGA ACT ACC ACT AAC TAC Ala Val Tyr Ile Arg Asn Glu Leu Tyr Ile Arg Thr Thr Thr Asn Tyr	400
90 95 100	
ATT GTA GCA TTT TGT GTT GTC CAC AAG AAT ACT CAA CCA TTC ATC GAA Ile Val Ala Phe Cys Val Val His Lys Asn Thr Gln Pro Phe Ile Glu	448
105 110 115	
AAG TAC TTC AAC AAA GCA GTA CTT TTG CCT AAT GAC TTA CTG GAA GTC Lys Tyr Phe Asn Lys Ala Val Leu Leu Pro Asn Asp Leu Leu Glu Val	496
120 125 130 135	
TGT GAA TTT GCA TAG GTT CTC TAT ATT TTT GAT GCA ACT GAA TTC AAA Cys Glu Phe Ala Gln Val Leu Tyr Ile Phe Asp Ala Thr Glu Phe Lys	544
140 145 150	
AAT TTG TAT CTT GAT AGG ATA CTT TCA TAA GAT ATT CGT AAG GAA CTC Asn Leu Tyr Leu Asp Arg Ile Leu Ser Gln Asp Ile Arg Lys Glu Leu	592
155 160 165	
ACT TTC CGT AAG TGT TTA CAA AGA TGC GTC AGA AGC AAG TTT TCT GAA Thr Phe Arg Lys Cys Leu Gln Arg Cys Val Arg Ser Lys Phe Ser Glu	640
170 175 180	
TTC AAC GAA TAC TAA CTT GGT AAG TAT TGC ACT GAA TCC TAA CGT AAG Phe Asn Glu Tyr Gln Leu Gly Lys Tyr Cys Thr Glu Ser Gln Arg Lys	688
185 190 195	
AAA ACA ATG TTC CGT TAC CTC TCA GTT ACC AAC AAG TAA AAG TGG GAT Lys Thr Met Phe Arg Tyr Leu Ser Val Thr Asn Lys Gln Lys Trp Asp	736
200 205 210 215	
TAA ACT AAG AAG AAG AGA AAA GAG AAT CTC TTA ACC AAA CTT TAG GCA Gln Thr Lys Lys Lys Arg Lys Glu Asn Leu Leu Thr Lys Leu Gln Ala	784
220 225 230	
ATA AAG GAA TCT GAA GAT AAG TCC AAG AGA GAA ACT GGA GAC ATA ATG Ile Lys Glu Ser Glu Asp Lys Ser Lys Arg Glu Thr Gly Asp Ile Met	832
235 240 245	

AAC GTT GAA GAT GCA ATC AAG GCT TTA AAA CCA GCA GTT ATG AAG AAA Asn Val Glu Asp Ala Ile Lys Ala Leu Lys Pro Ala Val Met Lys Lys 250 255 260	880
ATA GCC AAG AGA TAG AAT GCC ATG AAG AAA CAC ATG AAG GCA CCT AAA Ile Ala Lys Arg Gln Asn Ala Met Lys Lys His Met Lys Ala Pro Lys 265 270 275	928
ATT CCT AAC TCT ACC TTG GAA TCA AAG TAC TTG ACC TTC AAG GAT CTC Ile Pro Asn Ser Thr Leu Glu Ser Lys Tyr Leu Thr Phe Lys Asp Leu 280 285 290 295	976
ATT AAG TTC TGC CAT ATT TCT GAG CCT AAA GAA AGA GTC TAT AAG ATC Ile Lys Phe Cys His Ile Ser Glu Pro Lys Glu Arg Val Tyr Lys Ile 300 305 310	1024
CTT GGT AAA AAA TAC CCT AAG ACC GAA GAG GAA TAC AAA GCA GCC TTT Leu Gly Lys Lys Tyr Pro Lys Thr Glu Glu Glu Tyr Lys Ala Ala Phe 315 320 325	1072
GGT GAT TCT GCA TCT GCA CCC TTC AAT CCT GAA TTG GCT GGA AAG CGT Gly Asp Ser Ala Ser Ala Pro Phe Asn Pro Glu Leu Ala Gly Lys Arg 330 335 340	1120
ATG AAG ATT GAA ATC TCT AAA ACA TGG GAA AAT GAA CTC AGT GCA AAA Met Lys Ile Glu Ile Ser Lys Thr Trp Glu Asn Glu Leu Ser Ala Lys 345 350 355	1168
GGC AAC ACT GCT GAG GTT TGG GAT AAT TTA ATT TCA AGC AAT TAA CTC Gly Asn Thr Ala Glu Val Trp Asp Asn Leu Ile Ser Ser Asn Gln Leu 360 365 370 375	1216
CCA TAT ATG GCC ATG TTA CGT AAC TTG TCT AAC ATC TTA AAA GCC GGT Pro Tyr Met Ala Met Leu Arg Asn Leu Ser Asn Ile Leu Lys Ala Gly 380 385 390	1264
GTT TCA GAT ACT ACA CAC TCT ATT GTG ATC AAC AAG ATT TGT GAG CCC Val Ser Asp Thr Thr His Ser Ile Val Ile Asn Lys Ile Cys Glu Pro 395 400 405	1312
AAG GCC GTT GAG AAC TCC AAG ATG TTC CCT CTT CAA TTC TTT AGT GCC Lys Ala Val Glu Asn Ser Lys Met Phe Pro Leu Gln Phe Phe Ser Ala 410 415 420	1360
ATT GAA GCT GTT AAT GAA GCA GTT ACT AAG GGA TTC AAG GCC AAG AAG Ile Glu Ala Val Asn Glu Ala Val Thr Lys Gly Phe Lys Ala Lys Lys 425 430 435	1408
AGA GAA AAT ATG AAT CTT AAA GGT CAA ATC GAA GCA GTA AAG GAA GTT Arg Glu Asn Met Asn Leu Lys Gly Gln Ile Glu Ala Val Lys Glu Val 440 445 450 455	1456
GTT GAA AAA ACC GAT GAA GAG AAG AAA GAT ATG GAG TTG GAG TAA ACC Val Glu Lys Thr Asp Glu Glu Lys Lys Asp Met Glu Leu Glu Gln Thr 460 465 470	1504
GAA GAA GGA GAA TTT GTT AAA GTC AAC GAA GGA ATT GGC AAG CAA TAC Glu Glu Gly Glu Phe Val Lys Val Asn Glu Gly Ile Gly Lys Gln Tyr 475 480 485	1552

ATT AAC TCC ATT GAA CTT GCA ATC AAG ATA GCA GTT AAC AAG AAT TTA Ile Asn Ser Ile Glu Leu Ala Ile Lys Ile Ala Val Asn Lys Asn Leu 490 495 500	1600
GAT GAA ATC AAA GGA CAC ACT GCA ATC TTC TCT GAT GTT TCT GGT TCT Asp Glu Ile Lys Gly His Thr Ala Ile Phe Ser Asp Val Ser Gly Ser 505 510 515	1648
ATG AGT ACC TCA ATG TCA GGT GGA GCC AAG AAG TAT GGT TCC GTT CGT Met Ser Thr Ser Met Ser Gly Gly Ala Lys Lys Tyr Gly Ser Val Arg 520 525 530 535	1696
ACT TGT CTC GAG TGT GCA TTA GTC CTT GGT TTG ATG GTA AAA TAA CGT Thr Cys Leu Glu Cys Ala Leu Val Leu Gly Leu Met Val Lys Gln Arg 540 545 550	1744
TGT GAA AAG TCC TCA TTC TAC ATC TTC AGT TCA CCT AGT TCT CAA TGC Cys Glu Lys Ser Ser Phe Tyr Ile Phe Ser Ser Pro Ser Ser Gln Cys 555 560 565	1792
AAT AAG TGT TAC TTA GAA GTT GAT CTC CCT GGA GAC GAA CTC CGT CCT Asn Lys Cys Tyr Leu Glu Val Asp Leu Pro Gly Asp Glu Leu Arg Pro 570 575 580	1840
TCT ATG TAA AAA CTT TTG CAA GAG AAA GGA AAA CTT GGT GGT GGT ACT Ser Met Gln Lys Leu Leu Gln Glu Lys Gly Lys Leu Gly Gly Gly Thr 585 590 595	1888
GAT TTC CCC TAT GAG TGC ATT GAT GAA TGG ACA AAG AAT AAA ACT CAC Asp Phe Pro Tyr Glu Cys Ile Asp Glu Trp Thr Lys Asn Lys Thr His 600 605 610 615	1936
GTA GAC AAT ATC GTT ATT TTG TCT GAT ATG ATG ATT GCA GAA GGA TAT Val Asp Asn Ile Val Ile Leu Ser Asp Met Met Ile Ala Glu Gly Tyr 620 625 630	1984
TCA GAT ATC AAT GTT AGA GGC AGT TCC ATT GTT AAC AGC ATC AAA AAG Ser Asp Ile Asn Val Arg Gly Ser Ser Ile Val Asn Ser Ile Lys Lys 635 640 645	2032
TAC AAG GAT GAA GTA AAT CCT AAC ATT AAA ATC TTT GCA GTT GAC TTA Tyr Lys Asp Glu Val Asn Pro Asn Ile Lys Ile Phe Ala Val Asp Leu 650 655 660	2080
GAA GGT TAC GGA AAG TGC CTT AAT CTA GGT GAT GAG TTC AAT GAA AAC Glu Gly Tyr Gly Lys Cys Leu Asn Leu Gly Asp Glu Phe Asn Glu Asn 665 670 675	2128
AAC TAC ATC AAG ATA TTC GGT ATG AGC GAT TCA ATC TTA AAG TTC ATT Asn Tyr Ile Lys Ile Phe Gly Met Ser Asp Ser Ile Leu Lys Phe Ile 680 685 690 695	2176
TCA GCC AAG CAA GGA GGA GCA AAT ATG GTC GAA GTT ATC AAA AAC TTT Ser Ala Lys Gln Gly Gly Ala Asn Met Val Glu Val Ile Lys Asn Phe 700 705 710	2224
GCC CTT CAA AAA ATA GGA CAA AAG TGAGTTTCTT GAGATTCTTC TATAACAAAA Ala Leu Gln Lys Ile Gly Gln Lys 715	2278

ATCTCACCCC ACTTTTTTGT TTTATTGCAT AGCCATTATG AAATTTAAAT TATTATCTAT 2338
 TTATTTAAGT TACTTACATA GTTTATGTAT CGCAGTCTAT TAGCCTATTC AAATGATTCT 2398
 GCAAAGAACA AAAAAGATTA AAA 2421

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Glu Ile Glu Asn Asn Gln Ala Gln Gln Pro Lys Ala Glu Lys Leu
 1 5 10 15
 Trp Trp Glu Leu Glu Leu Glu Met Gln Glu Asn Gln Asn Asp Ile Gln
 20 25 30
 Val Arg Val Lys Ile Asp Asp Pro Lys Gln Tyr Leu Val Asn Val Thr
 35 40 45
 Ala Ala Cys Leu Leu Gln Glu Gly Ser Tyr Tyr Gln Asp Lys Asp Glu
 50 55 60
 Arg Arg Tyr Ile Ile Thr Lys Ala Leu Leu Glu Val Ala Glu Ser Asp
 65 70 75 80
 Pro Glu Phe Ile Cys Gln Leu Ala Val Tyr Ile Arg Asn Glu Leu Tyr
 85 90 95
 Ile Arg Thr Thr Thr Asn Tyr Ile Val Ala Phe Cys Val Val His Lys
 100 105 110
 Asn Thr Gln Pro Phe Ile Glu Lys Tyr Phe Asn Lys Ala Val Leu Leu
 115 120 125
 Pro Asn Asp Leu Leu Glu Val Cys Glu Phe Ala Gln Val Leu Tyr Ile
 130 135 140
 Phe Asp Ala Thr Glu Phe Lys Asn Leu Tyr Leu Asp Arg Ile Leu Ser
 145 150 155 160
 Gln Asp Ile Arg Lys Glu Leu Thr Phe Arg Lys Cys Leu Gln Arg Cys
 165 170 175
 Val Arg Ser Lys Phe Ser Glu Phe Asn Glu Tyr Gln Leu Gly Lys Tyr
 180 185 190
 Cys Thr Glu Ser Gln Arg Lys Lys Thr Met Phe Arg Tyr Leu Ser Val
 195 200 205
 Thr Asn Lys Gln Lys Trp Asp Gln Thr Lys Lys Lys Arg Lys Glu Asn
 210 215 220

Leu Leu Thr Lys Leu Gln Ala Ile Lys Glu Ser Glu Asp Lys Ser Lys
 225 230 235 240
 Arg Glu Thr Gly Asp Ile Met Asn Val Glu Asp Ala Ile Lys Ala Leu
 245 250 255
 Lys Pro Ala Val Met Lys Lys Ile Ala Lys Arg Gln Asn Ala Met Lys
 260 265 270
 Lys His Met Lys Ala Pro Lys Ile Pro Asn Ser Thr Leu Glu Ser Lys
 275 280 285
 Tyr Leu Thr Phe Lys Asp Leu Ile Lys Phe Cys His Ile Ser Glu Pro
 290 295 300
 Lys Glu Arg Val Tyr Lys Ile Leu Gly Lys Lys Tyr Pro Lys Thr Glu
 305 310 315 320
 Glu Glu Tyr Lys Ala Ala Phe Gly Asp Ser Ala Ser Ala Pro Phe Asn
 325 330 335
 Pro Glu Leu Ala Gly Lys Arg Met Lys Ile Glu Ile Ser Lys Thr Trp
 340 345 350
 Glu Asn Glu Leu Ser Ala Lys Gly Asn Thr Ala Glu Val Trp Asp Asn
 355 360 365
 Leu Ile Ser Ser Asn Gln Leu Pro Tyr Met Ala Met Leu Arg Asn Leu
 370 375 380
 Ser Asn Ile Leu Lys Ala Gly Val Ser Asp Thr Thr His Ser Ile Val
 385 390 395 400
 Ile Asn Lys Ile Cys Glu Pro Lys Ala Val Glu Asn Ser Lys Met Phe
 405 410 415
 Pro Leu Gln Phe Phe Ser Ala Ile Glu Ala Val Asn Glu Ala Val Thr
 420 425 430
 Lys Gly Phe Lys Ala Lys Lys Arg Glu Asn Met Asn Leu Lys Gly Gln
 435 440 445
 Ile Glu Ala Val Lys Glu Val Val Glu Lys Thr Asp Glu Glu Lys Lys
 450 455 460
 Asp Met Glu Leu Glu Gln Thr Glu Glu Gly Glu Phe Val Lys Val Asn
 465 470 475 480
 Glu Gly Ile Gly Lys Gln Tyr Ile Asn Ser Ile Glu Leu Ala Ile Lys
 485 490 495
 Ile Ala Val Asn Lys Asn Leu Asp Glu Ile Lys Gly His Thr Ala Ile
 500 505 510
 Phe Ser Asp Val Ser Gly Ser Met Ser Thr Ser Met Ser Gly Gly Ala
 515 520 525
 Lys Lys Tyr Gly Ser Val Arg Thr Cys Leu Glu Cys Ala Leu Val Leu
 530 535 540

Gly Leu Met Val Lys Gln Arg Cys Glu Lys Ser Ser Phe Tyr Ile Phe
 545 550 555 560
 Ser Ser Pro Ser Ser Gln Cys Asn Lys Cys Tyr Leu Glu Val Asp Leu
 565 570 575
 Pro Gly Asp Glu Leu Arg Pro Ser Met Gln Lys Leu Leu Gln Glu Lys
 580 585 590
 Gly Lys Leu Gly Gly Gly Thr Asp Phe Pro Tyr Glu Cys Ile Asp Glu
 595 600 605
 Trp Thr Lys Asn Lys Thr His Val Asp Asn Ile Val Ile Leu Ser Asp
 610 615 620
 Met Met Ile Ala Glu Gly Tyr Ser Asp Ile Asn Val Arg Gly Ser Ser
 625 630 635 640
 Ile Val Asn Ser Ile Lys Lys Tyr Lys Asp Glu Val Asn Pro Asn Ile
 645 650 655
 Lys Ile Phe Ala Val Asp Leu Glu Gly Tyr Gly Lys Cys Leu Asn Leu
 660 665 670
 Gly Asp Glu Phe Asn Glu Asn Asn Tyr Ile Lys Ile Phe Gly Met Ser
 675 680 685
 Asp Ser Ile Leu Lys Phe Ile Ser Ala Lys Gln Gly Gly Ala Asn Met
 690 695 700
 Val Glu Val Ile Lys Asn Phe Ala Leu Gln Lys Ile Gly Gln Lys
 705 710 715

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2829 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 47..2665
- (D) OTHER INFORMATION: /codon= (seq: "taa", aa: Gln)
 /codon= (seq: "tag", aa: Gln)
 /note= "Tetrahymena thermophila 95 kD
 TRT protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TCAATACTAT TAATTAATAA ATAAAAAAAAA GCAAACTACA AAGAAA ATG TCA AGG
 Met Ser Arg

55

CGT AAC TAA AAA AAG CCA TAG GCT CCT ATA GGC AAT GAA ACA AAT CTT Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu Thr Asn Leu 5 10 15	103
GAT TTT GTA TTA CAA AAT CTA GAA GTT TAC AAA AGC CAG ATT GAG CAT Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln Ile Glu His 20 25 30 35	151
TAT AAG ACC TAG TAG TAA TAG ATC AAA GAG GAG GAT CTC AAG CTT TTA Tyr Lys Thr Gln Gln Gln Gln Ile Lys Glu Glu Asp Leu Lys Leu Leu 40 45 50	199
AAG TTC AAA AAT TAA GAT TAG GAT GGA AAC TCT GGC AAC GAT GAT GAT Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn Asp Asp Asp 55 60 65	247
GAT GAA GAA AAC AAC TCA AAT AAA TAA TAA GAA TTA TTA AGG AGA GTC Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu Arg Arg Val 70 75 80	295
AAT TAG ATT AAG TAG CAA GTT TAA TTG ATA AAA AAA GTT GGT TCT AAG Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val Gly Ser Lys 85 90 95	343
GTA GAG AAA GAT TTG AAT TTG AAC GAA GAT GAA AAC AAA AAG AAT GGA Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys Lys Asn Gly 100 105 110 115	391
CTT TCT GAA TAG CAA GTG AAA GAA GAG TAA TTA AGA ACG ATT ACT GAA Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr Ile Thr Glu 120 125 130	439
GAA TAG GTT AAG TAT TAA AAT TTA GTA TTT AAC ATG GAC TAC CAG TTA Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp Tyr Gln Leu 135 140 145	487
GAT TTA AAT GAG AGT GGT GGC CAT AGA AGA CAC AGA AGA GAA ACA GAT Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg Glu Thr Asp 150 155 160	535
TAT GAT ACT GAA AAA TGG TTT GAA ATA TCT CAT GAC CAA AAA AAT TAT Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln Lys Asn Tyr 165 170 175	583
GTA TCA ATT TAC GCC AAC TAA AAG ACA TCA TAT TGT TGG TGG CTT AAA Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp Trp Leu Lys 180 185 190 195	631
GAT TAT TTT AAT AAA AAC AAT TAT GAT CAT CTT AAT GTA AGC ATT AAC Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val Ser Ile Asn 200 205 210	679
AGA CTA GAA ACT GAA GCC GAA TTC TAT GCC TTT GAT GAT TTT TCA CAA Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp Phe Ser Gln 215 220 225	727
ACA ATC AAA CTT ACT AAT AAT TCT TAC TAG ACT GTT AAC ATA GAC GTT Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn Ile Asp Val 230 235 240	775

AAT TTT GAT AAT AAT CTC TGT ATA CTC GCA TTG CTT AGA TTT TTA TTA Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg Phe Leu Leu 245 250 255	823
TCA CTA GAA AGA TTC AAT ATT TTG AAT ATA AGA TCT TCT TAT ACA AGA Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser Tyr Thr Arg 260 265 270 275	871
AAT TAA TAT AAT TTT GAG AAA ATT GGT GAG CTA CTT GAA ACT ATC TTC Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu Thr Ile Phe 280 285 290	919
GCA GTT GTC TTT TCT CAT CGC CAC TTA CAA GGC ATT CAT TTA CAA GTT Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His Leu Gln Val 295 300 305	967
CCT TGC GAA GCG TTC TAA TAT TTA GTT AAC TCC TCA TCA TAA ATT AGC Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser Gln Ile Ser 310 315 320	1015
GTT AAA GAT AGC TAA TTA TAG GTA TAC TCT TTC TCT ACA GAC TTA AAA Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr Asp Leu Lys 325 330 335	1063
TTA GTT GAC ACT AAC AAA GTC CAA GAT TAT TTT AAG TTC TTA TAA GAA Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe Leu Gln Glu 340 345 350 355	1111
TTC CCT CGT TTG ACT CAT GTA AGC TAG TAG GCT ATC CCA GTT AGT GCT Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro Val Ser Ala 360 365 370	1159
ACT AAC GCT GTA GAG AAC CTC AAT GTT TTA CTT AAA AAG GTC AAG CAT Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys Val Lys His 375 380 385	1207
GCT AAT CTT AAT TTA GTT TCT ATC CCT ACC TAA TTC AAT TTT GAT TTC Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn Phe Asp Phe 390 395 400	1255
TAC TTT GTT AAT TTA TAA CAT TTG AAA TTA GAG TTT GGA TTA GAA CCA Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly Leu Glu Pro 405 410 415	1303
AAT ATT TTG ACA AAA CAA AAG CTT GAA AAT CTA CTT TTG AGT ATA AAA Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Ser Ile Lys 420 425 430 435	1351
TAA TCA AAA AAT CTT AAA TTT TTA AGA TTA AAC TTT TAC ACC TAC GTT Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr Thr Tyr Val 440 445 450	1399
GCT TAA GAA ACC TCC AGA AAA CAG ATA TTA AAA CAA GCT ACA ACA ATC Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala Thr Thr Ile 455 460 465	1447
AAA AAT CTC AAA AAC AAT AAA AAT CAA GAA GAA ACT CCT GAA ACT AAA Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro Glu Thr Lys 470 475 480	1495

GAT GAA ACT CCA AGC GAA AGC ACA AGT GGT ATG AAA TTT TTT GAT CAT Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe Phe Asp His 485 490 495	1543
CTT TCT GAA TTA ACC GAG CTT GAA GAT TTC AGC GTT AAC TTG TAA GCT Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn Leu Gln Ala 500 505 510 515	1591
ACC CAA GAA ATT TAT GAT AGC TTG CAC AAA CTT TTG ATT AGA TCA ACA Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile Arg Ser Thr 520 525 530	1639
AAT TTA AAG AAG TTC AAA TTA AGT TAC AAA TAT GAA ATG GAA AAG AGT Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met Glu Lys Ser 535 540 545	1687
AAA ATG GAT ACA TTC ATA GAT CTT AAG AAT ATT TAT GAA ACC TTA AAC Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu Thr Leu Asn 550 555 560	1735
AAT CTT AAA AGA TGC TCT GTT AAT ATA TCA AAT CCT CAT GGA AAC ATT Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His Gly Asn Ile 565 570 575	1783
TCT TAT GAA CTG ACA AAT AAA GAT TCT ACT TTT TAT AAA TTT AAG CTG Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys Phe Lys Leu 580 585 590 595	1831
ACC TTA AAC TAA GAA TTA TAA CAC GCT AAG TAT ACT TTT AAG TAG AAC Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe Lys Gln Asn 600 605 610	1879
GAA TTT TAA TTT AAT AAC GTT AAA AGT GCA AAA ATT GAA TCT TCC TCA Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu Ser Ser Ser 615 620 625	1927
TTA GAA AGC TTA GAA GAT ATT GAT AGT CTT TGC AAA TCT ATT GCT TCT Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser Ile Ala Ser 630 635 640	1975
TGT AAA AAT TTA CAA AAT GTT AAT ATT ATC GCC AGT TTG CTC TAT CCC Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu Leu Tyr Pro 645 650 655	2023
AAC AAT ATT TAG AAA AAT CCT TTC AAT AAG CCC AAT CTT CTA TTT TTC Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu Leu Phe Phe 660 665 670 675	2071
AAG CAA TTT GAA TAA TTG AAA AAT TTG GAA AAT GTA TCT ATC AAC TGT Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser Ile Asn Cys 680 685 690	2119
ATT CTT GAT CAG CAT ATA CTT AAT TCT ATT TCA GAA TTC TTA GAA AAG Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe Leu Glu Lys 695 700 705	2167
AAT AAA AAA ATA AAA GCA TTC ATT TTG AAA AGA TAT TAT TTA TTA CAA Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr Leu Leu Gln 710 715 720	2215

TAT TAT CTT GAT TAT ACT AAA TTA TTT AAA ACA CTT CAA TAG TTA CCT Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln Gln Leu Pro 725 730 735	2263
GAA TTA AAT TAA GTT TAC ATT AAT TAG CAA TTA GAA GAA TTG ACT GTG Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu Leu Thr Val 740 745 750 755	2311
AGT GAA GTA CAT AAG TAA GTA TGG GAA AAC CAC AAG CAA AAA GCT TTC Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln Lys Ala Phe 760 765 770	2359
TAT GAA CCA TTA TGT GAG TTT ATC AAA GAA TCA TCC TAA ACC CTT TAG Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln Thr Leu Gln 775 780 785	2407
CTA ATA GAT TTT GAC CAA AAC ACT GTA AGT GAT GAC TCT ATT AAA AAG Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser Ile Lys Lys 790 795 800	2455
ATT TTA GAA TCT ATA TCT GAG TCT AAG TAT CAT CAT TAT TTG AGA TTG Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr Leu Arg Leu 805 810 815	2503
AAC CCT AGT TAA TCT AGC AGT TTA ATT AAA TCT GAA AAC GAA GAA ATT Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn Glu Glu Ile 820 825 830 835	2551
TAA GAA CTT CTC AAA GCT TGC GAC GAA AAA GGT GTT TTA GTA AAA GCA Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu Val Lys Ala 840 845 850	2599
TAC TAT AAA TTC CCT CTA TGT TTA CCA ACT GGT ACT TAT TAC GAT TAC Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr Tyr Asp Tyr 855 860 865	2647
AAT TCA GAT AGA TGG TGATTAATTA AATATTAGTT TAAATAAATA TTAAATATTG Asn Ser Asp Arg Trp 870	2702
AATATTTCTT TGCTTATTAT TTGAATAATA CATACAATAG TCATTTTGTAG TGTTTTGAAT	2762
ATATTTTAGT TATTTAATTC ATTATTTTAA GTAAATAATT ATTTTTCAT CATTTTGTAA	2822
AAAATCG	2829

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Ser Arg Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu
1 5 10 15

Thr Asn Leu Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln
 20 25 30
 Ile Glu His Tyr Lys Thr Gln Gln Gln Gln Ile Lys Glu Glu Asp Leu
 35 40 45
 Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn
 50 55 60
 Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu
 65 70 75 80
 Arg Arg Val Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val
 85 90 95
 Gly Ser Lys Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys
 100 105 110
 Lys Asn Gly Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr
 115 120 125
 Ile Thr Glu Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp
 130 135 140
 Tyr Gln Leu Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg
 145 150 155 160
 Glu Thr Asp Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln
 165 170 175
 Lys Asn Tyr Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp
 180 185 190
 Trp Leu Lys Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val
 195 200 205
 Ser Ile Asn Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp
 210 215 220
 Phe Ser Gln Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn
 225 230 235 240
 Ile Asp Val Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg
 245 250 255
 Phe Leu Leu Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser
 260 265 270
 Tyr Thr Arg Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu
 275 280 285
 Thr Ile Phe Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His
 290 295 300
 Leu Gln Val Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser
 305 310 315 320
 Gln Ile Ser Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr
 325 330 335

Asp Leu Lys Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe
 340 345 350
 Leu Gln Glu Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro
 355 360 365
 Val Ser Ala Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys
 370 375 380
 Val Lys His Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn
 385 390 395 400
 Phe Asp Phe Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly
 405 410 415
 Leu Glu Pro Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Leu
 420 425 430
 Ser Ile Lys Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr
 435 440 445
 Thr Tyr Val Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala
 450 455 460
 Thr Thr Ile Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro
 465 470 475 480
 Glu Thr Lys Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe
 485 490 495
 Phe Asp His Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn
 500 505 510
 Leu Gln Ala Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile
 515 520 525
 Arg Ser Thr Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met
 530 535 540
 Glu Lys Ser Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu
 545 550 555 560
 Thr Leu Asn Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His
 565 570 575
 Gly Asn Ile Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys
 580 585 590
 Phe Lys Leu Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe
 595 600 605
 Lys Gln Asn Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu
 610 615 620
 Ser Ser Ser Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser
 625 630 635 640
 Ile Ala Ser Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu
 645 650 655

Leu Tyr Pro Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu
 660 665 670
 Leu Phe Phe Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser
 675 680 685
 Ile Asn Cys Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe
 690 695 700
 Leu Glu Lys Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr
 705 710 715 720
 Leu Leu Gln Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln
 725 730 735
 Gln Leu Pro Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu
 740 745 750
 Leu Thr Val Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln
 755 760 765
 Lys Ala Phe Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln
 770 775 780
 Thr Leu Gln Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser
 785 790 795 800
 Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr
 805 810 815
 Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn
 820 825 830
 Glu Glu Ile Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu
 835 840 845
 Val Lys Ala Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr
 850 855 860
 Tyr Asp Tyr Asn Ser Asp Arg Trp
 865 870

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 884 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..884
- (D) OTHER INFORMATION: /note= "Saccharomyces cerevisiae
L8543.12 (Est2p) protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Lys Ile Leu Phe Glu Phe Ile Gln Asp Lys Leu Asp Ile Asp Leu
 1 5 10 15
 Gln Thr Asn Ser Thr Tyr Lys Glu Asn Leu Lys Cys Gly His Phe Asn
 20 25 30
 Gly Leu Asp Glu Ile Leu Thr Thr Cys Phe Ala Leu Pro Asn Ser Arg
 35 40 45
 Lys Ile Ala Leu Pro Cys Leu Pro Gly Asp Leu Ser His Lys Ala Val
 50 55 60
 Ile Asp His Cys Ile Ile Tyr Leu Leu Thr Gly Glu Leu Tyr Asn Asn
 65 70 75 80
 Val Leu Thr Phe Gly Tyr Lys Ile Ala Arg Asn Glu Asp Val Asn Asn
 85 90 95
 Ser Leu Phe Cys His Ser Ala Asn Val Asn Val Thr Leu Leu Lys Gly
 100 105 110
 Ala Ala Trp Lys Met Phe His Ser Leu Val Gly Thr Tyr Ala Phe Val
 115 120 125
 Asp Leu Leu Ile Asn Tyr Thr Val Ile Gln Phe Asn Gly Gln Phe Phe
 130 135 140
 Thr Gln Ile Val Gly Asn Arg Cys Asn Glu Pro His Leu Pro Pro Lys
 145 150 155 160
 Trp Val Gln Arg Ser Ser Ser Ser Ser Ala Thr Ala Ala Gln Ile Lys
 165 170 175
 Gln Leu Thr Glu Pro Val Thr Asn Lys Gln Phe Leu His Lys Leu Asn
 180 185 190
 Ile Asn Ser Ser Ser Phe Phe Pro Tyr Ser Lys Ile Leu Pro Ser Ser
 195 200 205
 Ser Ser Ile Lys Lys Leu Thr Asp Leu Arg Glu Ala Ile Phe Pro Thr
 210 215 220
 Asn Leu Val Lys Ile Pro Gln Arg Leu Lys Val Arg Ile Asn Leu Thr
 225 230 235 240
 Leu Gln Lys Leu Leu Lys Arg His Lys Arg Leu Asn Tyr Val Ser Ile
 245 250 255
 Leu Asn Ser Ile Cys Pro Pro Leu Glu Gly Thr Val Leu Asp Leu Ser
 260 265 270
 His Leu Ser Arg Gln Ser Pro Lys Glu Arg Val Leu Lys Phe Ile Ile
 275 280 285
 Val Ile Leu Gln Lys Leu Leu Pro Gln Glu Met Phe Gly Ser Lys Lys
 290 295 300
 Asn Lys Gly Lys Ile Ile Lys Asn Leu Asn Leu Leu Leu Ser Leu Pro
 305 310 315 320

Leu Asn Gly Tyr Leu Pro Phe Asp Ser Leu Leu Lys Lys Leu Arg Leu
 325 330 335
 Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys His
 340 345 350
 Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp Leu
 355 360 365
 Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr
 370 375 380
 Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr Trp
 385 390 395 400
 Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr Leu
 405 410 415
 Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser Asn
 420 425 430
 Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu
 435 440 445
 Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe
 450 455 460
 Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln Lys
 465 470 475 480
 Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys Ile
 485 490 495
 Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln Arg
 500 505 510
 Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met Lys
 515 520 525
 Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys Met
 530 535 540
 Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val Arg
 545 550 555 560
 Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn
 565 570 575
 Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu Leu Tyr Ile Asp
 580 585 590
 Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val
 595 600 605
 Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr
 610 615 620
 Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile
 625 630 635 640

Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys
 645 650 655
 Ala Ser Pro Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe
 660 665 670
 Leu Ile Ile Ser Thr Asp Gln Gln Gln Val Ile Asn Ile Lys Lys Leu
 675 680 685
 Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys
 690 695 700
 Ile Leu Ala Val Ser Ser Gln Ser Asp Asp Asp Thr Val Ile Gln Phe
 705 710 715 720
 Cys Ala Met His Ile Phe Val Lys Glu Leu Glu Val Trp Lys His Ser
 725 730 735
 Ser Thr Met Asn Asn Phe His Ile Arg Ser Lys Ser Ser Lys Gly Ile
 740 745 750
 Phe Arg Ser Leu Ile Ala Leu Phe Asn Thr Arg Ile Ser Tyr Lys Thr
 755 760 765
 Ile Asp Thr Asn Leu Asn Ser Thr Asn Thr Val Leu Met Gln Ile Asp
 770 775 780
 His Val Val Lys Asn Ile Ser Glu Cys Tyr Lys Ser Ala Phe Lys Asp
 785 790 795 800
 Leu Ser Ile Asn Val Thr Gln Asn Met Gln Phe His Ser Phe Leu Gln
 805 810 815
 Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp
 820 825 830
 Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu
 835 840 845
 Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu
 850 855 860
 Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile
 865 870 875 880
 His Ile Val Asn

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

DGTDATNARN ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu	Cys	Val	Ser	Tyr	Ile	Leu	Ser	Ser	Phe	Tyr	Tyr	Ala	Asn	Leu	Glu
1			5						10					15	
Glu	Asn	Ala	Leu	Gln	Phe	Leu	Arg	Lys	Glu	Ser	Met	Asp	Pro	Glu	Lys
			20					25					30		
Pro	Glu	Thr	Asn	Leu	Leu	Met	Arg	Leu	Thr						
			35				40								

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Leu	Cys	Val	Ser	Ser	Ile	Leu	Ser	Ser	Phe	Tyr	Tyr	Ala	Thr	Leu	Glu
1			5						10					15	

Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn
 20 25 30
 Pro Asn Val Asn Leu Leu Met Arg Leu Thr
 35 40

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
 /note= "N = thymidine modified by a
 biotin group"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 12..13
- (D) OTHER INFORMATION: /mod_base= gm

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 14..17
- (D) OTHER INFORMATION: /mod_base= um

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 18..21
- (D) OTHER INFORMATION: /mod_base= gm

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 22..25
- (D) OTHER INFORMATION: /mod_base= um

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 26
- (D) OTHER INFORMATION: /mod_base= gm

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

NAGACCTGTT ANNNNNNNNNN NNNNNN

26

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGGGTTTTGG GGT TTT

16

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..389
- (D) OTHER INFORMATION: /note= "partial sequence of a cDNA encoding human telomerase peptide motifs (EST AA281296)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCCAAGTTCC TGC ACTGGCT GATGAGTGTG TACGTCGTCG AGCTGCTCAG GTCTTTCTTT	60
TATGTCACGG AGACCACGTT TCAAAAGAAC AGGCTCTTTT TCTACCGGAA GAGTGTCTGG	120
AGCAAGTTGC AAAGCATTGG AATCAGACAG CACTTGAAGA GGGTGCAGCT GCGGGACGTG	180
TCGGAAGCAG AGGTCAGGCA GCATCGGGAA GCCAGGCCCG CCCTGCTGAC GTCCAGACTC	240
CGCTTCATCC CCAAGCCTGA CGGGCTGCGG CCGATTGTGA ACATGGACTA CGTCGTGGGA	300
GCCAGAACGT TCCGCAGAGA AAAGAGGGCC GAGCGTCTCA CCTCGAGGGT GAAGGCACTG	360
TTCAGCGTGC TCAACTACGA GCGGGCGCG	389

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```

Ile Ser Glu Ile Glu Trp Leu Val Leu Gly Lys Arg Ser Asn Ala Lys
1           5           10           15

Met Cys Leu Ser Asp Phe Glu Lys Arg Lys Gln Ile Phe Ala Glu Phe
          20           25           30

Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe
          35           40           45

Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe
          50           55           60

Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met
65           70           75           80

Lys Met Glu Ala Phe Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp
          85           90           95

Thr Gln Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys
          100          105          110

Lys Asn Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile
          115          120          125

Lys Met Gly Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu
          130          135          140

Arg Pro Val Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser
145          150          155          160

Gly Ile Pro Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys
          165          170          175

Lys Asp Leu Leu Lys His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val
          180          185          190

Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met
          195          200          205

Phe Arg Ile Val Lys Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg
          210          215          220

Lys Tyr Ala Thr Ile His Ala Thr Ser
225          230

```

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

Leu Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys
1           5           10           15

```

His Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp
 20 25 30
 Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys
 35 40 45
 Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr
 50 55 60
 Trp Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr
 65 70 75 80
 Leu Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser
 85 90 95
 Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn
 100 105 110
 Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu
 115 120 125
 Phe Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln
 130 135 140
 Lys Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys
 145 150 155 160
 Ile Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln
 165 170 175
 Arg Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met
 180 185 190
 Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys
 195 200 205
 Met Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val
 210 215 220
 Arg Ser Gln Tyr Phe Phe Asn Thr Asn
 225 230

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Thr Arg Glu Ile Ser Trp Met Gln Val Glu Thr Ser Ala Lys His Phe
 1 5 10 15

Tyr Tyr Phe Asp His Glu Asn Ile Tyr Val Leu Trp Lys Leu Leu Arg
 20 25 30
 Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
 35 40 45
 Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
 50 55 60
 Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp Leu Lys Lys
 65 70 75 80
 Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu Glu Trp Lys Lys
 85 90 95
 Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr
 100 105 110
 Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val Asn Ser Asp
 115 120 125
 Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu Leu Asn Ser His
 130 135 140
 Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys Asp Pro Phe Gly
 145 150 155 160
 Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys Tyr Glu Glu Phe
 165 170 175
 Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu Phe Phe Ala Thr
 180 185 190
 Met Asp Ile Glu Lys Cys Tyr Asp Ser Val Asn Arg Glu Lys Leu Ser
 195 200 205
 Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser Ser Asp Phe Trp Ile Met
 210 215 220
 Thr Ala Gln Ile Leu Lys Arg Lys Asn
 225 230

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2631
- (D) OTHER INFORMATION: /note= "Saccharomyces cerevisiae Est 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATTTATACTC ATGAAAATCT TATTTCGAGTT CATTCAAGAC AAGCTTGACA TTGATCTACA	60
GACCAACAGT ACTTACAAAG AAAATTTAAA ATGTGGTCAC TTCAATGGCC TCGATGAAAT	120
TCTAACTACG TGTTCGCAC TACCAAATTC AAGAAAAATA GCATTACCAT GCCTTCCTGG	180
TGACTTAAGC CACAAAGCAG TCATTGATCA CTGCATCATT TACCTGTTGA CGGGCGAATT	240
ATACAACAAC GTACTAACAT TTGGCTATAA AATAGCTAGA AATGAAGATG TCAACAATAG	300
TCTTTTTTGC CATTCTGCAA ATGTTAACGT TACGTTACTG AAAGGCGCTG CTTGGAAAAT	360
GTTCCACAGT TTGGTCGGTA CATACGCATT CGTTGATTTA TTGATCAATT ATACAGTAAT	420
TCAATTTAAT GGGCAGTTTT TCACTCAAAT CGTGGGTAAC AGATGTAACG AACCTCATCT	480
GCCGCCCAA TGGGTCCAAC GATCATCCTC ATCATCCGCA ACTGCTGCGC AAATCAAACA	540
ACTTACAGAA CCAGTGACAA ATAAACAATT CTTACACAAG CTCAATATAA ATTCCTCTTC	600
TTTTTTTCCT TATAGCAAGA TCCTTCCTTC ATCATCATCT ATCAAAAAGC TAACTGACTT	660
GAGAGAAGCT ATTTTTCCCA CAAATTTGGT TAAAATTCCT CAGAGACTAA AGGTACGAAT	720
TAATTTGACG CTGCAAAAGC TATTAAAGAG ACATAAGCGT TTGAATTACG TTTCTATTTT	780
GAATAGTATT TGCCCACCAT TGGAAGGGAC CGTATTGGAC TTGTCGCATT TGAGTAGGCA	840
ATCACCAAAG GAACGAGTCT TGAAATTTAT CATTGTTATT TTACAGAAGT TATTACCCCA	900
AGAAATGTTT GGCTCAAAGA AAAATAAAGG AAAAAATTAT AAGAACTAA ATCTTTTATT	960
AAGTTTACCC TTAAATGGCT ATTTACCATT TGATAGTTTG TTGAAAAAGT TAAGATTAAA	1020
GGATTTTCGG TGGTTGTTCA TTTCTGATAT TTGGTTCACC AAGCACAATT TTGAAAACCT	1080
GAATCAATTG GCGATTTGTT TCATTTCTTG GCTATTTAGA CAACTAATTC CCAAATATAT	1140
ACAGACTTTT TTTTACTGCA CCGAAATATC TTCTACAGTG ACAATTGTTT ACTTTAGACA	1200
TGATACTTGG AATAAACTTA TCACCCCTTT TATCGTAGAA TATTTTAAGA CGTACTTAGT	1260
CGAAAACAAC GTATGTAGAA ACCATAATAG TTACACGTTG TCCAATTTCA ATCATAGCAA	1320
AATGAGGATT ATACCAAAAA AAAGTAATAA TGAGTTCAGG ATTATTGCCA TCCCATGCAG	1380
AGGGGCAGAC GAAGAAGAAT TCACAATTTA TAAGGAGAAT CACAAAAATG CTATCCAGCC	1440
CACTCAAAAA ATTTTAGAAT ACCTAAGAAA CAAAAGGCCG ACTAGTTTTA CTAAAATATA	1500
TTCTCCAACG CAAATAGCTG ACCGTATCAA AGAATTTAAG CAGAGACTTT TAAAGAAATT	1560
TAATAATGTC TTACCAGAGC TTTATTTTAT GAAATTTGAT GTCAAATCTT GCTATGATTC	1620
CATACCAAGG ATGGAATGTA TGAGGATACT CAAGGATGCG CTAAAAAATG AAAATGGGTT	1680
TTTCGTTAGA TCTCAATATT TCTTCAATAC CAATACAGGT GTATTGAAGT TATTTAATGT	1740
TGTTAACGCT AGCAGAGTAC CAAAACCTTA TGAGCTATAC ATAGATAATG TGAGGACGGT	1800

TCATTTATCA AATCAGGATG TTATAAACGT TGTAGAGATG GAAATATTTA AAACAGCTTT	1860
GTGGGTTGAA GATAAGTGCT ACATTAGAGA AGATGGTCTT TTTCAGGGCT CTAGTTTATC	1920
TGCTCCGATC GTTGATTTGG TGTATGACGA TCTTCTGGAG TTTTATAGCG AGTTTAAAGC	1980
CAGTCCTAGC CAGGACACAT TAATTTTAAA ACTGGCTGAC GATTTCCTTA TAATATCAAC	2040
AGACCAACAG CAAGTGATCA ATATCAAAAA GCTTGCCATG GGCGGATTTT AAAAATATAA	2100
TGCGAAAGCC AATAGAGACA AAATTTTAGC CGTAAGCTCC CAATCAGATG ATGATACGGT	2160
TATTCAATTT TGTGCAATGC ACATATTTGT TAAAGAATTG GAAGTTTGGA AACATTCAAG	2220
CACAATGAAT AATTTCCATA TCCGTTTCGAA ATCTAGTAAA GGGATATTTT GAAGTTTAAAT	2280
AGCGCTGTTT AACACTAGAA TCTCTTATAA AACAATTGAC ACAAATTTAA ATTCAACAAA	2340
CACCGTTCTC ATGCAAATTG ATCATGTTGT AAAGAACATT TCGGAATGTT ATAAATCTGC	2400
TTTTAAGGAT CTATCAATTA ATGTTACGCA AAATATGCAA TTTCATTCGT TCTTACAACG	2460
CATCATTGAA ATGACAGTCA GCGGTTGTCC AATTACGAAA TGTGATCCTT TAATCGAGTA	2520
TGAGGTACGA TTCACCATAT TGAATGGATT TTTGGAAAGC CTATCTTCAA ACACATCAAA	2580
ATTTAAAGAT AATATCATTC TTTTGAGAAA GGAAATTCAA CACTTGCAAG C	2631

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ala	Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu
1				5					10					15	
Arg	Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu
			20					25					30		
Phe	Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile
		35					40					45			
Arg	Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu
		50				55					60				
Val	Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu
65				70						75				80	
Arg	Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp
			85						90					95	

Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg
 100 105 110

Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg
 115 120 125

Ala

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(959..1216, 1273..1353, 1425..1543, 1595
 ..1857, 1894..2286, 2326..2396, 2436..2705, 2746
 ..2862, 2914..3083, 3125..3309, 3356..3504, 3546
 ..3759, 3797..4046, 4086..4252, 4296..4392, 4435
 ..4594)
- (D) OTHER INFORMATION: /note= "Saccharomyces pombe telomerase
 catalytic subunit (TRT)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGTACCGATT TACTTTCCTT TCTTCATAAG CTAATTGCTT CCTCGAACGC TCCTAAATCT	60
CTGGAAATAT TTTTACAAGA ACTCAATAAC AATACCAAGT CAAATTCCAA TATGAAGGTG	120
TTATTAGTGA TCGATAATAT TTCTATTTTA TCGGTCGTTA CCAAGTATAA GGACAAAAAG	180
AACAACTTCC TTCCCCCTAA AGACTTTTAC TTTATTAATT TACTTTTCAA ATATATTTTCG	240
GGTTCGCTTA CTTTAAATCG TGGTACTGTT TTAGCTGCTA CTTCTAGCCA ACCGCGTGTT	300
TCTACCCCGT CATTGGATAT AGCTCTTGGA GTAGCTCACA GAAATCCTTA CAAATCTTCT	360
GATGAGACTA TATTAGATTC ATTACAGTCC GTGCATATTC TTAACATGGA GCCTTACACT	420
TTAGATGAGT CACGTCGCAT GATGGAGTAT TTGGTATCAT CCAACGTTTG CCTTGAAAAG	480
GTTGATAATT ATTTGCAAAA TCATGTCCTT AGTGGTGGTA ATCCGCGAAA GTTTTTTGAT	540
GCTTGCACAC GTCTAGCATG ATTGAGATAT TCAAAAATTT CTATCCACTA CAACTCCTTT	600
AACGCGGTTT TATTTTTCTA TTTTCTATTC TCATGTTGTT CCAAATATGT ATCATCTCGT	660
ATTAGGCTTT TTTCCGTTTT ACTCCTGGAA TCGTACCTTT TTTACTATTC CCCCTAATGA	720
ATAATCTAAA TTAGTTTCGC TTATAATTGA TAGTAGTAGA AAGATTGGTG ATTCTACTCG	780
TGTAATGTTA TTAGTTTAAA GATACTTTGC AAAACATTTA TTAGCTATCA TTATATAAAA	840

AAAATCCTAT AATTATAAAT ATTAATCAAT ATTTGCGGTC ACTATTTATT TAAAACGTTA	900
TGATCAGTAG GACACTTTGC ATATATATAG TTATGCTTAA TGGTTACTTG TAACTTGC	958
ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu 1 5 10 15	1006
AAT CAA TAT GTA TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val 20 25 30	1054
TTG AGA GGG TCG CCG GCA AGC TCG TAT AGC AAT ATA TGC GAA CGC TTG Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu 35 40 45	1102
AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT CAT TCG ACT GTA Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val 50 55 60	1150
GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro 65 70 75 80	1198
AAA TGC TCA CAG TCA GAG GTATATATAT TTTTGTTTTG ATTTTTTTCT Lys Cys Ser Gln Ser Glu 85	1246
ATTCGGGATA GCTAATATAT GGGCAG CTA ATA GCG AAT GTT GTA AAA CAG ATG Leu Ile Ala Asn Val Val Lys Gln Met 90 95	1299
TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA CTG ATG AAA GGG TTT Phe Asp Glu Ser Phe Glu Arg Arg Arg Asn Leu Leu Met Lys Gly Phe 100 105 110	1347
TCC ATG GTAAGGTATT CTAATTGTGA AATATTTACC TGCAATTACT GTTTCAAAGA Ser Met	1403
GATTGTATTT AACCGATAAA G AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA Asn His Glu Asp Phe Arg Ala Met His Val 115 120	1454
AAC GGA GTA CAA AAT GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA Asn Gly Val Gln Asn Asp Leu Val Ser Thr Phe Pro Asn Tyr Leu Ile 125 130 135	1502
TCT ATA CTT GAG TCA AAA AAT TGG CAA CTT TTG TTA GAA AT Ser Ile Leu Glu Ser Lys Asn Trp Gln Leu Leu Leu Glu Ile 140 145 150	1543
GTAAATACCG GTTAAGATGT TGCGCACTTT GAACAAGACT GACAAGTATA G T ATC Ile	1598
GGC AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG Gly Ser Asp Ala Met His Tyr Leu Leu Ser Lys Gly Ser Ile Phe Glu 155 160 165 170	1646

GCT CTT CCA AAT GAC AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT Ala Leu Pro Asn Asp Asn Tyr Leu Gln Ile Ser Gly Ile Pro Leu Phe 175 180 185	1694
AAA AAT AAT GTG TTT GAG GAA ACT GTG TCA AAA AAA AGA AAG CGA ACC Lys Asn Asn Val Phe Glu Glu Thr Val Ser Lys Lys Arg Lys Arg Thr 190 195 200	1742
ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA GAA GTT TCC Ile Glu Thr Ser Ile Thr Gln Asn Lys Ser Ala Arg Lys Glu Val Ser 205 210 215	1790
TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC Trp Asn Ser Ile Ser Ile Ser Arg Phe Ser Ile Phe Tyr Arg Ser Ser 220 225 230	1838
TAT AAG AAG TTT AAG CAA G GTA ACTAATA CTGTTATCCT TCATAACTAA Tyr Lys Lys Phe Lys Gln 235 240	1887
TTTTAG AT CTA TAT TTT AAC TTA CAC TCT ATT TGT GAT CGG AAC ACA Asp Leu Tyr Phe Asn Leu His Ser Ile Cys Asp Arg Asn Thr 245 250	1934
GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG CAA TTT GGA CTT ATA Val His Met Trp Leu Gln Trp Ile Phe Pro Arg Gln Phe Gly Leu Ile 255 260 265 270	1982
AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA TCA Asn Ala Phe Gln Val Lys Gln Leu His Lys Val Ile Pro Leu Val Ser 275 280 285	2030
CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT Gln Ser Thr Val Val Pro Lys Arg Leu Leu Lys Val Tyr Pro Leu Ile 290 295 300	2078
GAA CAA ACA GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC Glu Gln Thr Ala Lys Arg Leu His Arg Ile Ser Leu Ser Lys Val Tyr 305 310 315	2126
AAC CAT TAT TGC CCA TAT ATT GAC ACC CAC GAT GAT GAA AAA ATC CTT Asn His Tyr Cys Pro Tyr Ile Asp Thr His Asp Asp Glu Lys Ile Leu 320 325 330	2174
AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG TTT CTT CGA TCC ATT Ser Tyr Ser Leu Lys Pro Asn Gln Val Phe Ala Phe Leu Arg Ser Ile 335 340 345 350	2222
CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA TTT Leu Val Arg Val Phe Pro Lys Leu Ile Trp Gly Asn Gln Arg Ile Phe 355 360 365	2270
GAG ATA ATA TTA AAA G GTATTGTATA AAATTTATTA CCACTAACGA TTTTACCAG AC 2327 Glu Ile Ile Leu Lys 370	Asp
CTC GAA ACT TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT Leu Glu Thr Phe Leu Lys Leu Ser Arg Tyr Glu Ser Phe Ser Leu His 375 380 385	2375

TAT TTA ATG AGT AAC ATA AAG GTAATATGCC AAATTTTTTTT ACCATTAATT 2426
 Tyr Leu Met Ser Asn Ile Lys
 390 395

AACAAATCAG ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA AAA AGG TCA 2474
 Ile Ser Glu Ile Glu Trp Leu Val Leu Gly Lys Arg Ser
 400 405

AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT 2522
 Asn Ala Lys Met Cys Leu Ser Asp Phe Glu Lys Arg Lys Gln Ile Phe
 410 415 420

GCG GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA 2570
 Ala Glu Phe Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu
 425 430 435 440

CAA TCT TTT TTT TAT ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT 2618
 Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr
 445 450 455

GTT TAT TTT AGA AAA GAT ATT TGG AAA CTC TTG TGC CGA CCC TTT ATT 2666
 Val Tyr Phe Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile
 460 465 470

ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG GTATTTTAAA 2715
 Thr Ser Met Lys Met Glu Ala Phe Glu Lys Ile Asn Glu
 475 480 485

GTATTTTTTTG CAAAAAGCTA ATATTTTCAG AAC AAT GTT AGG ATG GAT ACT CAG 2769
 Asn Asn Val Arg Met Asp Thr Gln
 490

AAA ACT ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT 2817
 Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn
 495 500 505

ACC TTT CGT CTC ATT ACG AAT TTA AGA AAA AGA TTC TTA ATA AAG 2862
 Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys
 510 515 520

GTATTAATTT TTGGTCATCA ATGTACTTTA CTTCTAATCT ATTATTAGCA G ATG GGT 2919
 Met Gly
 525

TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG 2967
 Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val
 530 535 540

GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA 3015
 Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro
 545 550 555

TTT AAC TTG GAG GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT 3063
 Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu
 560 565 570

CTT AAG CAC CGA ATG TTT GG GTAATTATAT AATGCGCGAT TCCTCATTAT 3113
 Leu Lys His Arg Met Phe Gly
 575 580

TAATTTTGCA G G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA AAA TCC	3161
Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser	
585 590	
TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG	3209
Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys Lys	
595 600 605	
AAA CTC AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT	3257
Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile His	
610 615 620 625	
GCA ACA AGT GAC CGA GCT ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC	3305
Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe Ser	
630 635 640	
TAT T GTAAGTTTAT TTTTTCATTG GAATTTTTTA ACAAATTCTT TTTTAG TT	3357
Tyr Phe	
GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA	3405
Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser Met Lys Thr	
645 650 655	
TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT	3453
Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr Lys Ser Ser	
660 665 670 675	
TCT GAA ATT TTT AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT	3501
Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly His Ile Val	
680 685 690	
AAG GTATACCAAT TGTGAATTG TAATAACACT AATGAACTA G ATA GGA AAT	3554
Lys Ile Gly Asn	
695	
TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA ATT CTG TCA	3602
Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser	
700 705 710	
TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA	3650
Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu	
715 720 725	
TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT	3698
Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp	
730 735 740	
TTC CTC TTT ATA ACA GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT	3746
Phe Leu Phe Ile Thr Val Asn Lys Lys Asp Ala Lys Lys Phe Leu Asn	
745 750 755	
TTA TCT TTA AGA G GTGAGTTGCT GTCATTCCTA AGTTCTAACC GTTGAAG GA	3798
Leu Ser Leu Arg Gly	
760	
TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA ATA AAC	3846
Phe Glu Lys His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn	
765 770 775 780	

TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC Phe Glu Asn Ser Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser 785 790 795	3894
AAG AAA AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu 800 805 810	3942
GAT ACA TTG TTA GCA TGT CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT Asp Thr Leu Leu Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser 815 820 825	3990
ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG AAA TCT TTT TTT TAC AAA Thr Ser Val Glu Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys 830 835 840	4038
ATT CTA AG GTATACTGTG TAACTGAATA ATAGCTGACA AATAATCAG A TCG Ile Leu Arg Ser 845	4089
AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser 850 855 860	4137
AAA TTC AAT TCT TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys 865 870 875 880	4185
ATG AGA GCA CAA GCA TAC TTA AAA AGG ATG AAG GAT ATA TTT ATT CCC Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro 885 890 895	4233
CAA AGA ATG TTC ATA ACG G GTGAGTACTT ATTTTAACTA GAAAAGTCAT Gln Arg Met Phe Ile Thr 900	4282
TAATTAACCT TAG AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA Asp Leu Leu Asn Val Ile Gly Arg Lys Ile Trp Lys 905 910	4330
AAG TTG GCC GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu Ser Ser 915 920 925 930	4378
GCA GAA GTC AAA TG GTACGTGTCTG GTCTCGAGAC TTCAGCAATA TTGACACATC Ala Glu Val Lys Trp 935	4432
AG G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA CCC TCT TTC AAA Leu Phe Cys Leu Gly Met Arg Asp Gly Leu Lys Pro Ser Phe Lys 940 945 950	4480
TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr Gln Phe Gln Ser Leu Thr 955 960 965	4528
GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA Asp Leu Ile Lys Pro Leu Arg Pro Val Leu Arg Gln Val Leu Phe Leu 970 975 980	4576

CAT AGA AGA ATA GCT GAT TAATGTCATT TTCAATTTAT TATATACATC 4624
His Arg Arg Ile Ala Asp
985

CTTTATTACT GGTGTCTTAA ACAATATTAT TACTAAGTAT AGCTGACCCC CAAAGCAAGC 4684
ATACTATAGG ATTTCTAGTA AAGTAAAATT AATCTCGTTA TTAGTTTTGA TTGACTTGTC 4744
TTTATCCTTA TACTTTTAAG AAAGATTGAC AGTGGTTGCT GACTACTGCC CACATGCCCA 4804
TTAAACGGGA GTGGTTAAAC ATTAAAAGTA ATACATGAGG CTAATCTCCT TTCATTTAGA 4864
ATAAGGAAAG TGGTTTTCTA TAATGAATAA TGCCCGCACT AATGCAAAAA GACGAAGATT 4924
ATCTTCTAAA CAAGGGGGAT TAAGCATATC CGAAGGAAAA GAGAGTAATA TACCCAGTGT 4984
TGTTGAAGAA AGCAAGGATA ATTTGGAACA AGCTTCTGCA GATGACAGGC TAAATTTTGG 5044
TGACCGAATT TTGGTAAAAG CCCCAGGTTA TCCATGGTGG CCGGCCTTGC TACTGAGACC 5104
AAAAGAACT AAGGATAGTT TGAATACTAA TAGCTCATTT AATGTCTTAT ATAAGGTTTT 5164
GTTTTTTCCT GACTTCAATT TTGCATGGGT GAAAAGAAAT AGTGTTAAGC CATTATTGGA 5224
TTCCGAAATA GCCAAATTTT TTGGTTCCTC AAAGCGGAAG TCTAAAGAAC TTATTGAAGC 5284
TTATGAGGCT TCAAAAACCT CTCCTGATTT AAAGGAGGAA TCTTCCACCG ATGAGGAAAT 5344
GGATAGCTTA TCAGCTGCTG AGGAGAAGCC TAATTTTTTTG CAAAAAAGAA AATATCATTG 5404
GGAGACATCT CTTGATGAAT CAGATGCGGA GAGTATCTCC AGCGGATCCT TGATGTCAAT 5464
AACTTCTATT TCTGAAATGT ATGGTCCTAC TGTCGCTTCG ACTTCTCGTA GCTCTACGCA 5524
GTTAAGTGAC CAAAGGTACC 5544

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 988 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met	Thr	Glu	His	His	Thr	Pro	Lys	Ser	Arg	Ile	Leu	Arg	Phe	Leu	Glu
1				5					10					15	
Asn	Gln	Tyr	Val	Tyr	Leu	Cys	Thr	Leu	Asn	Asp	Tyr	Val	Gln	Leu	Val
			20					25					30		
Leu	Arg	Gly	Ser	Pro	Ala	Ser	Ser	Tyr	Ser	Asn	Ile	Cys	Glu	Arg	Leu
		35					40					45			
Arg	Ser	Asp	Val	Gln	Thr	Ser	Phe	Ser	Ile	Phe	Leu	His	Ser	Thr	Val
	50					55					60				

Val	Gly	Phe	Asp	Ser	Lys	Pro	Asp	Glu	Gly	Val	Gln	Phe	Ser	Ser	Pro	65	70	75	80
Lys	Cys	Ser	Gln	Ser	Glu	Leu	Ile	Ala	Asn	Val	Val	Lys	Gln	Met	Phe	85	90	95	
Asp	Glu	Ser	Phe	Glu	Arg	Arg	Arg	Asn	Leu	Leu	Met	Lys	Gly	Phe	Ser	100	105	110	
Met	Asn	His	Glu	Asp	Phe	Arg	Ala	Met	His	Val	Asn	Gly	Val	Gln	Asn	115	120	125	
Asp	Leu	Val	Ser	Thr	Phe	Pro	Asn	Tyr	Leu	Ile	Ser	Ile	Leu	Glu	Ser	130	135	140	
Lys	Asn	Trp	Gln	Leu	Leu	Leu	Glu	Ile	Ile	Gly	Ser	Asp	Ala	Met	His	145	150	155	160
Tyr	Leu	Leu	Ser	Lys	Gly	Ser	Ile	Phe	Glu	Ala	Leu	Pro	Asn	Asp	Asn	165	170	175	
Tyr	Leu	Gln	Ile	Ser	Gly	Ile	Pro	Leu	Phe	Lys	Asn	Asn	Val	Phe	Glu	180	185	190	
Glu	Thr	Val	Ser	Lys	Lys	Arg	Lys	Arg	Thr	Ile	Glu	Thr	Ser	Ile	Thr	195	200	205	
Gln	Asn	Lys	Ser	Ala	Arg	Lys	Glu	Val	Ser	Trp	Asn	Ser	Ile	Ser	Ile	210	215	220	
Ser	Arg	Phe	Ser	Ile	Phe	Tyr	Arg	Ser	Ser	Tyr	Lys	Lys	Phe	Lys	Gln	225	230	235	240
Asp	Leu	Tyr	Phe	Asn	Leu	His	Ser	Ile	Cys	Asp	Arg	Asn	Thr	Val	His	245	250	255	
Met	Trp	Leu	Gln	Trp	Ile	Phe	Pro	Arg	Gln	Phe	Gly	Leu	Ile	Asn	Ala	260	265	270	
Phe	Gln	Val	Lys	Gln	Leu	His	Lys	Val	Ile	Pro	Leu	Val	Ser	Gln	Ser	275	280	285	
Thr	Val	Val	Pro	Lys	Arg	Leu	Leu	Lys	Val	Tyr	Pro	Leu	Ile	Glu	Gln	290	295	300	
Thr	Ala	Lys	Arg	Leu	His	Arg	Ile	Ser	Leu	Ser	Lys	Val	Tyr	Asn	His	305	310	315	320
Tyr	Cys	Pro	Tyr	Ile	Asp	Thr	His	Asp	Asp	Glu	Lys	Ile	Leu	Ser	Tyr	325	330	335	
Ser	Leu	Lys	Pro	Asn	Gln	Val	Phe	Ala	Phe	Leu	Arg	Ser	Ile	Leu	Val	340	345	350	
Arg	Val	Phe	Pro	Lys	Leu	Ile	Trp	Gly	Asn	Gln	Arg	Ile	Phe	Glu	Ile	355	360	365	
Ile	Leu	Lys	Asp	Leu	Glu	Thr	Phe	Leu	Lys	Leu	Ser	Arg	Tyr	Glu	Ser	370	375	380	

Phe Ser Leu His Tyr Leu Met Ser Asn Ile Lys Ile Ser Glu Ile Glu
 385 390 395 400
 Trp Leu Val Leu Gly Lys Arg Ser Asn Ala Lys Met Cys Leu Ser Asp
 405 410 415
 Phe Glu Lys Arg Lys Gln Ile Phe Ala Glu Phe Ile Tyr Trp Leu Tyr
 420 425 430
 Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr Ile Thr Glu
 435 440 445
 Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys Asp Ile Trp
 450 455 460
 Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met Lys Met Glu Ala Phe
 465 470 475 480
 Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp Thr Gln Lys Thr Thr
 485 490 495
 Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg
 500 505 510
 Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys Met Gly Ser Asn
 515 520 525
 Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val Ala Ser
 530 535 540
 Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro Phe Asn
 545 550 555 560
 Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu Leu Lys
 565 570 575
 His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys
 580 585 590
 Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys
 595 600 605
 Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile
 610 615 620
 His Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe
 625 630 635 640
 Ser Tyr Phe Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser
 645 650 655
 Met Lys Thr Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr
 660 665 670
 Lys Ser Ser Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly
 675 680 685
 His Ile Val Lys Ile Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile
 690 695 700

Pro	Gln	Gly	Ser	Ile	Leu	Ser	Ser	Phe	Leu	Cys	His	Phe	Tyr	Met	Glu	705	710	715	720
Asp	Leu	Ile	Asp	Glu	Tyr	Leu	Ser	Phe	Thr	Lys	Lys	Lys	Gly	Ser	Val	725	730	735	
Leu	Leu	Arg	Val	Val	Asp	Asp	Phe	Leu	Phe	Ile	Thr	Val	Asn	Lys	Lys	740	745	750	
Asp	Ala	Lys	Lys	Phe	Leu	Asn	Leu	Ser	Leu	Arg	Gly	Phe	Glu	Lys	His	755	760	765	
Asn	Phe	Ser	Thr	Ser	Leu	Glu	Lys	Thr	Val	Ile	Asn	Phe	Glu	Asn	Ser	770	775	780	
Asn	Gly	Ile	Ile	Asn	Asn	Thr	Phe	Phe	Asn	Glu	Ser	Lys	Lys	Arg	Met	785	790	795	800
Pro	Phe	Phe	Gly	Phe	Ser	Val	Asn	Met	Arg	Ser	Leu	Asp	Thr	Leu	Leu	805	810		815
Ala	Cys	Pro	Lys	Ile	Asp	Glu	Ala	Leu	Phe	Asn	Ser	Thr	Ser	Val	Glu	820	825		830
Leu	Thr	Lys	His	Met	Gly	Lys	Ser	Phe	Phe	Tyr	Lys	Ile	Leu	Arg	Ser	835	840		845
Ser	Leu	Ala	Ser	Phe	Ala	Gln	Val	Phe	Ile	Asp	Ile	Thr	His	Asn	Ser	850	855		860
Lys	Phe	Asn	Ser	Cys	Cys	Asn	Ile	Tyr	Arg	Leu	Gly	Tyr	Ser	Met	Cys	865	870	875	880
Met	Arg	Ala	Gln	Ala	Tyr	Leu	Lys	Arg	Met	Lys	Asp	Ile	Phe	Ile	Pro	885	890		895
Gln	Arg	Met	Phe	Ile	Thr	Asp	Leu	Leu	Asn	Val	Ile	Gly	Arg	Lys	Ile	900	905		910
Trp	Lys	Lys	Leu	Ala	Glu	Ile	Leu	Gly	Tyr	Thr	Ser	Arg	Arg	Phe	Leu	915	920		925
Ser	Ser	Ala	Glu	Val	Lys	Trp	Leu	Phe	Cys	Leu	Gly	Met	Arg	Asp	Gly	930	935	940	
Leu	Lys	Pro	Ser	Phe	Lys	Tyr	His	Pro	Cys	Phe	Glu	Gln	Leu	Ile	Tyr	945	950	955	960
Gln	Phe	Gln	Ser	Leu	Thr	Asp	Leu	Ile	Lys	Pro	Leu	Arg	Pro	Val	Leu	965	970		975
Arg	Gln	Val	Leu	Phe	Leu	His	Arg	Arg	Ile	Ala	Asp					980	985		

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 1

(D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = guanosine modified by a
biotin group"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

NCCTATTTYT TYTAYNNNAC NGA

23

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Phe	Phe	Tyr	Xaa	Thr	Glu
1				5	

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CCAGATATNA DNARRAARTC RTC

23

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe, Ile or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Asp Asp Phe Leu Xaa Ile
1 5

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ACAATGGMGNH TNHTNCCNAA RAA

23

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2..3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Arg Xaa Xaa Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ACGAATCKNG GDATNSWRTC RTARCA

26

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Cys Tyr Asp Ser Ile Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAATTCTCRT ARCANSWYTT DATRTC

26

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Asp Ile Lys Ser Cys Tyr Asp
1 5

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 269 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GATTACTCCC GAAGAAAGGA TCTTTCCGTC CAATCATGAC TTTCTTAAGA AAGGACAAGC	60
AAAAAAATAT TAAGTTAAAT CTAAATTAAA TTCTAATGGA TAGCCAACTT GTGTTTAGGA	120
ATTTAAAAGA CATGCTGGGA TAAAAGATAG GATACTCAGT CTTTGATAAT AAACAAATTT	180
CAGAAAAATT TGCCTAATTC ATAGAGAAAT GGAAAAATAA AGGAAGACCT CAGCTATATT	240
ATGTCACTCT AGACATAAAG ACTTGCTAC	269

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 474 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AAACACAAGG AAGGAAGTCA AATATTCTAT TACCGTAAAC CAATATGGAA ATTAGTGAGT	60
AAATTAAC TAAGTCAAAGT AAGAATTTAG TTTTCTGAAA AGAATAAATA AATGAAAAAT	120
AATTTTTATC AAAAAATTTA GCTTGAAGAG GAGAATTTGG AAAAAAGTTGA AGAAAAATTG	180
ATACCAGAAG ATTCATTTTA GAAATACCTT CAAGGAAAGC TAAGGATTAT ACCTAAAAAA	240
GGATCTTTCC GTCCAATCAT GACTTTCTTA AGAAAGGACA AGCAAAAAAA TATTAAGTTA	300
AATCTAAATT AAATTCTAAT GGATAGCCAA CTTGTGTTTA GGAATTTAAA AGACATGCTG	360
GGATAAAAGA TAGGATACTC AGTCTTTGAT AATAAACAAA TTTCAGAAAA ATTTGCCTAA	420
TTCATAGAGA AATGGAAAAA TAAAGGAAGA CCTCAGCTAT ATTATGTCAC TCTA	474

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ala Tyr Asp Thr Ile
1 5

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Phe Phe Tyr Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe
1 5 10 15

Arg His Asp Thr Trp Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr
20 25 30

Phe Lys Thr Tyr Leu Val Glu Asn Asn Val Cys Arg Asn His Asn Ser
35 40 45

Tyr Thr Leu Ser Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys
50 55 60

Lys Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala
65 70 75 80

Asp Glu Glu Glu Phe Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile
85 90 95

Gln Pro Thr Gln Lys Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr
100 105 110

Ser Phe Thr Lys Ile Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys
115 120 125

Glu Phe Lys Gln Arg Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu
130 135 140

Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr
 1 5 10 15
 Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp
 20 25 30
 Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu Glu
 35 40 45
 Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro
 50 55 60
 Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val
 65 70 75 80
 Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu Leu
 85 90 95
 Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys Asp
 100 105 110
 Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys Tyr
 115 120 125
 Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu Phe
 130 135 140
 Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp
 145 150 155

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Lys His Lys Glu Gly Ser Gln Ile Phe Tyr Tyr Arg Lys Pro Ile Trp
 1 5 10 15
 Lys Leu Val Ser Lys Leu Thr Ile Val Lys Val Arg Ile Gln Phe Ser
 20 25 30
 Glu Lys Asn Lys Gln Met Lys Asn Asn Phe Tyr Gln Lys Ile Gln Leu
 35 40 45
 Glu Glu Glu Asn Leu Glu Lys Val Glu Glu Lys Leu Ile Pro Glu Asp
 50 55 60

Ser	Phe	Gln	Lys	Tyr	Pro	Gln	Gly	Lys	Leu	Arg	Ile	Ile	Pro	Lys	Lys
65					70					75					80
Gly	Ser	Phe	Arg	Pro	Ile	Met	Thr	Phe	Leu	Arg	Lys	Asp	Lys	Gln	Lys
			85						90					95	
Asn	Ile	Lys	Leu	Asn	Leu	Asn	Gln	Ile	Leu	Met	Asp	Ser	Gln	Leu	Val
			100					105					110		
Phe	Arg	Asn	Leu	Lys	Asp	Met	Leu	Gly	Gln	Lys	Ile	Gly	Tyr	Ser	Val
			115				120					125			
Phe	Asp	Asn	Lys	Gln	Ile	Ser	Glu	Lys	Phe	Ala	Gln	Phe	Ile	Glu	Lys
	130					135					140				
Trp	Lys	Asn	Lys	Gly	Arg	Pro	Gln	Leu	Tyr	Tyr	Val	Thr	Leu		
145					150					155					

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Gly Ile Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTGAAGGCAC TGTCAGCG

19

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTGGATGATT TCTTGTGG

19

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGCTCCTGC GTTTGGTGG

19

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CTGGACACTC AGCCCTTGG

19

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GGCAGGTGTG CTGGACACT

19

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TTTGATGATG CTGGCGATG

19

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGGGCTCGTC TTCTACAGG

19

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CAGCAGGAGG ATCTTG TAG

19

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TGACCCCAGG AGTGGCAGG

19

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TCAAGCTGAC TCGACACCG

19

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CGGCGTGACA GGGCTGC

17

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GCTGAAGGCT GAGTGTCC

18

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TAGTCCATGT TCACAATCG

19

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 22..1716
- (D) OTHER INFORMATION: /note= "DNA encoding ORF for 63 kD
hTERT protein from EcoRI-NotI insert of
clone 712562"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GCCAAGTTCC TGC	ACTGGCT G	ATG AGT GTG TAC GTC GTC GAG CTG CTC AGG	51
	Met Ser Val Tyr Val Val Glu Leu Leu Arg		
	1 5 10		
TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG CTC TTT		99	
Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe			
	15 20 25		
TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT GGA ATC AGA		147	
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg			
	30 35 40		
CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG GAA GCA GAG GTC		195	
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val			
	45 50 55		
AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG ACG TCC AGA CTC CGC		243	
Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg			
	60 65 70		
TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC		291	
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr			
	75 80 85 90		
GTC GTG GGA GCC AGA ACG TTC CGC AGA GAA AAG ARG GCC GAG CGT CTC		339	
Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Xaa Ala Glu Arg Leu			
	95 100 105		
ACC TCG AGG GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG		387	
Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala			
	110 115 120		
CGG CGC CCC GGC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC		435	
Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile			
	125 130 135		
CAC AGG GCC TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG		483	
His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro			
	140 145 150		

CCG CCT GAG CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC	531
Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp	
155 160 165 170	
ACC ATC CCC CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA	579
Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys	
175 180 185	
CCC CAG AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC	627
Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala	
190 195 200	
GCC ATG GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG	675
Ala Met Gly Thr Ser Ala Arg Pro Ser Arg Ala Thr Ser Tyr Val Gln	
205 210 215	
TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC	723
Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser	
220 225 230	
CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG CGG	771
Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg	
235 240 245 250	
GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG ACA CCT	819
Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro	
255 260 265	
CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC CGA GGT GTC	867
His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val	
270 275 280	
CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG AAG ACA GTG GTG AAC TTC	915
Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe	
285 290 295	
CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT TTT GTT CAG ATG CCG	963
Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro	
300 305 310	
GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG CTG CTG GAT ACC CGG ACC	1011
Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr	
315 320 325 330	
CTG GAG GTG CAG AGC GAC TAC TCC AGC TAT GCC CGG ACC TCC ATC AGA	1059
Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg	
335 340 345	
GCC AGT CTC ACC TTC AAC CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT	1107
Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg	
350 355 360	
CGC AAA CTC TTT GGG GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG	1155
Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu	
365 370 375	
GAT TTG CAG GTG AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG	1203
Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys	
380 385 390	

ATC CTC CTG CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC	1251
Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu	
395 400 405 410	
CCA TTT CAT CAG CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA	1299
Pro Phe His Gln Gln Val Trp Lys Asn Pro His Phe Ser Cys Ala Ser	
415 420 425	
TCT CTG ACA CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC	1347
Ser Leu Thr Arg Leu Pro Leu Leu Leu His Pro Glu Ser Gln Glu Arg	
430 435 440	
AGG GAT GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA	1395
Arg Asp Val Ala Gly Gly Gln Gly Arg Arg Arg Pro Ser Ala Leu Arg	
445 450 455	
GGC CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG	1443
Gly Arg Ala Val Ala Val Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser	
460 465 470	
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC CCA	1491
Thr Pro Cys His Leu Arg Ala Thr Pro Gly Val Thr Gln Asp Ser Pro	
475 480 485 490	
GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC CCT GGA	1539
Asp Ala Ala Glu Ser Glu Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly	
495 500 505	
GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC CAT CCT GGA	1587
Gly Arg Ser Gln Pro Gly Thr Ala Leu Arg Leu Gln Asp His Pro Gly	
510 515 520	
CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG ACA CCA GCA GCC	1635
Leu Met Ala Thr Arg Pro Gln Pro Gly Arg Glu Gln Thr Pro Ala Ala	
525 530 535	
CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG AGG GGC GGC CCA CAC	1683
Leu Ser Arg Arg Ala Tyr Thr Ser Gln Gly Gly Arg Gly Gly Pro His	
540 545 550	
CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC TGAGTGAGTG TTTGGCCGAG	1733
Pro Gly Leu His Arg Trp Glu Ser Glu Ala	
555 560	
GCCTGCATGT CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA	1793
GGGCTGAGTG TCCAGCACAC CTGCGTTTTT ACTTCCCCAC AGGCTGGCGT TCGGTCCACC	1853
CCAGGGCCAG CTTTTCTCA CCAGGAGCCC GGCTTCCACT CCCCACATAG GAATAGTCCA	1913
TCCCCAGATT CGCCATTGTT CACCCTTCGC CCTGCCTTCC TTTGCCTTCC ACCCCCACCA	1973
TTCAGGTGGA GACCCTGAGA AGGACCCTGG GAGCTTTGGG AATTTGGAGT GACCAAAGGT	2033
GTGCCCTGTA CACAGGCGAG GACCCTGCAC CTGGATGGGG GTCCCTGTGG GTCAAATTGG	2093
GGGGAGGTGC TGTGGGAGTA AAATACTGAA TATATGAGTT TTTCAGTTTT GGAAAAAAAA	2153
AAAAAAAAA AAAAAAAAA	2171

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

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Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr
 1           5           10           15
Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val
          20           25           30
Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val
          35           40           45
Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala
          50           55           60
Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp
          65           70           75           80
Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr
          85           90           95
Phe Arg Arg Glu Lys Xaa Ala Glu Arg Leu Thr Ser Arg Val Lys Ala
          100          105          110
Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu
          115          120          125
Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr
          130          135          140
Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe
          145          150          155          160
Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg
          165          170          175
Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys
          180          185          190
Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala Met Gly Thr Ser Ala
          195          200          205
Arg Pro Ser Arg Ala Thr Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
          210          215          220
Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
          225          230          235          240
Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg
          245          250          255
Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys
          260          265          270

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Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val
 275 280 285
 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala
 290 295 300
 Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro
 305 310 315 320
 Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp
 325 330 335
 Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn
 340 345 350
 Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val
 355 360 365
 Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser
 370 375 380
 Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala
 385 390 395 400
 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val
 405 410 415
 Trp Lys Asn Pro His Phe Ser Cys Ala Ser Ser Leu Thr Arg Leu Pro
 420 425 430
 Leu Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp Val Ala Gly Gly
 435 440 445
 Gln Gly Arg Arg Arg Pro Ser Ala Leu Arg Gly Arg Ala Val Ala Val
 450 455 460
 Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser Thr Pro Cys His Leu Arg
 465 470 475 480
 Ala Thr Pro Gly Val Thr Gln Asp Ser Pro Asp Ala Ala Glu Ser Glu
 485 490 495
 Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly Gly Arg Ser Gln Pro Gly
 500 505 510
 Thr Ala Leu Arg Leu Gln Asp His Pro Gly Leu Met Ala Thr Arg Pro
 515 520 525
 Gln Pro Gly Arg Glu Gln Thr Pro Ala Ala Leu Ser Arg Arg Ala Tyr
 530 535 540
 Thr Ser Gln Gly Gly Arg Gly Gly Pro His Pro Gly Leu His Arg Trp
 545 550 555 560
 Glu Ser Glu Ala

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCAGTGAGCA GAGTGACGAG GACTCGAGCT CAAGCTTTTT TTTTTTTTTT

50

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CCAGTGAGCA GAGTGACG

18

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAGGACTCGA GCTCAAGC

18

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CACTGATCCT TTCTTTTTCG TAAACGATAG GT

32

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CATCAATCAA ATCTTCATA TAGAAATGAC A

31

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = 5' phosphorylated guanosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

NGGCCGTGTT GGCCTAGTTC TCTGCTC

27

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAGGAGGAGA AGAGCAGAGA ACTAGGCCAA CACGCCCC

38

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GTGTCATTTT TATATGGAAG ATTTGATTGA TG

32

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

ACCTATCGTT TACGAAAAAG AAAGGATCAG TG

32

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAGTGACATA ATATACGTGA

20

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Phe Phe Tyr Val Thr Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..4029
- (D) OTHER INFORMATION: /note= "preliminary sequence of hTRT cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GCAGCGCTGC	GTCCTGCTGC	GCACGTGGGA	AGCCCTGGCC	CCGGCCACCC	CCGCGATGCC	60
GCGCGCTCCC	CGCTGCCGAG	CCGTGCGCTC	CCTGCTGCGC	AGCCACTACC	GCGAGGTGCT	120
GCCGCTGGCC	ACGTTTCGTG	GGCGCCTGGG	GCCCCAGGGC	TGGCGGCTGG	TGCAGCGCGG	180
GGACCCGGCG	GCTTTCCGCG	CGNTGGTGGC	CCANTGCNTG	GTGTGCGTGC	CCTGGGANGN	240
ANGGCNGCCC	CCCGCCGCCC	CCTCCTTCCG	CCAGGTGTCC	TGCCTGAANG	ANCTGGTGGC	300
CCGAGTGCTG	CANANGCTGT	GCGANCGCGG	CGCGAANAAC	GTGCTGGCCT	TCGGCTTCGC	360
GCTGCTGGAC	GGGGCCCGCG	GGGGCCCCCC	CGAGGCCTTC	ACCACCAGCG	TGCGCAGCTA	420
CCTGCCCAAC	ACGGTGACCG	ACGCACTGCG	GGGGAGCGGG	GCGTGGGGGC	TGCTGCTGCG	480
CCGCGTGGGC	GACGACGTGC	TGGTTCACCT	GCTGGCACGC	TGCGCGNTNT	TTGTGCTGGT	540
GGNTCCCAGC	TGCGCCTACC	ANGTGTGCGG	GCCGCCGCTG	TACCAGCTCG	GCGCTGCNAC	600
TCAGGCCCCG	CCCCCGCCAC	ACGCTANTGG	ACCCGAANGC	GTCTGGGATC	CAACGGGCCT	660
GGAACCATAG	CGTCAGGGAG	GCCGGGGTCC	CCCTGGGCTG	CCAGCCCCGG	GTGCGAGGAG	720
GCGCGGGGGC	AGTGCCAGCC	GAAGTCTGCC	GTTGCCCAAG	AGGCCCAGGC	GTGGCGCTGC	780
CCCTGAGCCG	GAGCGGACGC	CCGTGGGGCA	GGGGTCCTGG	GCCCACCCGG	GCAGGACGCC	840
TGGACCGAGT	GACCGTGGTT	TCTGTGTGGT	GTCACCTGCC	AGACCCGCCG	AAGAAGCCAC	900
CTCTTTGGAG	GGTGCGCTCT	CTGGCACGCG	CCACTCCCAC	CCATCCGTGG	GCCGCCAGCA	960
CCACGCGGGC	CCCCCATCCA	CATCGCGGCC	ACCACGTCCT	GGGACACGCC	TTGTCCCCCG	1020
GTGTACGCCG	AGACCAAGCA	CTTCCTCTAC	TCCTCAGGCG	ACAAGNACAC	TGCGNCCCTC	1080
CTTCCTACTC	AATATATCTG	AGGCCCAGCC	TGACTGGCGT	TCGGGAGGTT	CGTGGAGACA	1140
NTCTTTCTGG	TTCCAGGCCT	TGGATGCCAG	GATTCCCCGC	AGGTTGCCCC	GCCTGCCCCA	1200
GCGNCTACTG	CAAATGCGGC	CCCTGTTTCT	GGAGCTGCTT	GGGAACCACG	CGCAGTGCCC	1260
CTACGGGGTG	TTCTCAAGA	CGCACTGCCC	GCTGCGAGCT	GCGGTCACCC	CAGCAGCCGG	1320

TGTCTGTGCC	CGGGAGAAGC	CCCAGGGCTC	TGTGGCGGCC	CCCGAGGAGG	AGGAACACAG	1380
ACCCCCGTGC	CCTGGTGCAG	CTGCTCCGCC	AGCACAGCAG	CCCCTGGCAG	GTGTACGGCT	1440
TCGTGCGGGC	CTGCCTGCGC	CGGCTGGTGC	CCCCAGGCCT	CTGGGGCTCC	AGGCACAACG	1500
AACGCCGCTT	CCTCAGGAAC	ACCAAGAAGT	TCATCTCCCT	GGGGAAGCAT	GCCAAGCTCT	1560
CGCTGCAGGA	GCTGACGTGG	AAGATGAGCG	TGCGGGACTG	CGCTTGGCTG	CGCAGGAGCC	1620
CAGGGGTTGG	CTGTGTTCCG	GCCGCAGAGC	ACCGTCTGCG	TGAGGAGATC	CTGGCCAAGT	1680
TCCTGCACTG	GCTGATGAGT	GTGTACGTCG	TCGAGCTGCT	CAGGTCTTTC	TTTTATGTCA	1740
CGGAGACCAC	GTTTCAAAAG	AACAGGCTCT	TTTTCTACCG	GAAGAGTGTC	TGGAGCAAGT	1800
TGCAAAGCAT	TGGAATCAGA	CAGCACTTGA	AGAGGGTGCA	GCTGCGGGAG	CTGTCGGAAG	1860
CAGAGGTCAG	GCAGCATCGG	GAAGCCAGGC	CCGCCCTGCT	GACGTCCAGA	CTCCGCTTCA	1920
TCCCCAAGCC	TGACGGGCTG	CGGCCGATTG	TGAACATGGA	CTACGTCTGT	GGAGCCAGAA	1980
CGTTCCGCAG	AGAAAAGAGG	GCCGAGCGTC	TCACCTCGAG	GGTGAAGGCA	CTGTTACGCG	2040
TGCTCAACTA	CGAGCGGGCG	CGGCGCCCCG	GCCTCCTGGG	CGCCTCTGTG	CTGGGCCTGG	2100
ACGATATCCA	CAGGGCCTGG	CGCACCTTCG	TGCTGCGTGT	GCGGGCCCAG	GACCCGCCGC	2160
CTGAGCTGTA	CTTTGTCAAG	GTGGATGTGA	CGGGCGCGTA	CGACACCATC	CCCCAGGACA	2220
GGCTCACGGA	GGTCATCGCC	AGCATCATCA	AACCCAGAA	CACGTACTGC	GTGCGTCGGT	2280
ATGCCGTGGT	CCAGAAGGCC	GCCCATGGGC	ACGTCCGCAA	GGCCTTCAAG	AGCCACGTCT	2340
CTACCTTGAC	AGACCTCCAG	CCGTACATGC	GACAGTTCGT	GGCTCACCTG	CAGGANAACA	2400
GCCCGCTGAG	GGATGCCGTC	GTCATCGAGC	AGAGCTCCTC	CCTGAATGAG	GCCAGCAGTG	2460
GCCTCTTCGA	CGTCTTCTTA	CGCTTCATGT	GCCACCACGC	CGTGCGCATC	AGGGGCAAGT	2520
CCTACGTCCA	GTGCCAGGGG	ATCCCGCAGG	GCTCCATCCT	CTCCACGCTG	CTCTGCAGCC	2580
TGTGCTACGG	CGACATGGAG	AACAAGCTGT	TTGCGGGGAT	TCGGCGGGAC	GGGCTGCTCC	2640
TGCGTTTGGT	GGATGATTTC	TTGTTGGTGA	CACCTCACCT	CACCCACGCG	AAAACCTTCC	2700
TCAGGACCCT	GGTCCGAGGT	GTCCCTGAGT	ATGGCTGCGT	GGTGAACCTG	CGGAAGACAG	2760
TGGTGAACCT	CCCTGTAGAA	GACGAGGCCC	TGGGTGGCAC	GGCTTTTGTT	CAGATGCCGG	2820
CCCACGGCCT	ATTCCCCTGG	TGCGGCCTGC	TGCTGGATAC	CCGACCCTG	GAGGTGCAGA	2880
GCGACTACTC	CAGCTATGCC	CGGACCTCCA	TCAGAGCCAG	TCTCACCTTC	AACCGCGGCT	2940
TCAAGGCTGG	GAGGAACATG	CGTCGCAAAC	TCTTTGGGGT	CTTGCGGCTG	AAGTGTACACA	3000
GCCTGTTTCT	GGATTTGCAG	GTGAACAGCC	TCCAGACGGT	GTGCACCAAC	ATCTACAAGA	3060
TCCTCCTGCT	GCAGGCGTAC	AGGTTTCACG	CATGTGTGCT	GCAGCTCCCA	TTTCATCAGC	3120

AAGTTTGGAA GAACCCACACA TTTTTCCTGC GCGTCATCTC TGACACGGCC TCCCTCTGCT	3180
ACTCCATCCT GAAAGCCAAG AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC	3240
CTCTGCCCTC CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCCTGCTC AAGCTGACTC	3300
GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACCTCAG GACAGCCCAG ACGCAGCTGA	3360
GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC CGCAGCCAAC CCGGCACTGC	3420
CCTCAGACTT CAAGACCATC CTGGACTGAT GGCCACCCGC CCACAGCCAG GCCGAGAGCA	3480
GACACCAGCA GCCCTGTCAC GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCCACAC	3540
CCAGGCCCCG ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT	3600
CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA GGGCTGAGTG	3660
TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG CTCGGCTCCA CCCAGGGCC	3720
AGCTTTTCCT CACCAGGAGC CCGGCTTCCA CTCCCCACAT AGGAATAGTC CATCCCCAGA	3780
TTCGCCATTG TTCACCCCTC GCCCTGCCCT CCTTTGCCTT CCACCCCCAC CATCCAGGTG	3840
GAGACCCTGA GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG	3900
TACACAGGCG AGGACCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT GGGGGGAGGT	3960
GCTGTGGGAG TAAAATACTG AATATATGAG TTTTTCAGTT TTGAAAAAAAA AAAAAAAAAA	4020
AAAAAAAAA	4029

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Arg or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 10
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ile or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 12
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Thr or Ser"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Xaa Xaa Xaa Xaa Xaa Asp Asp Xaa Leu Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 18
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

Lys Xaa Tyr Xaa Gln Xaa Xaa Gly Ile Pro Gln Gly Ser Xaa Leu Ser
1 5 10 15

Xaa Xaa Leu Xaa Xaa Xaa Tyr Xaa Asp Leu
20 25

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 7
      (D) OTHER INFORMATION: /product= "OTHER"
                               /note= "Xaa = hydrophobic amino acid,
                                     selected from Ala, Leu Ile, Val, Pro,
                                     Phe, Trp or Met"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 8
      (D) OTHER INFORMATION: /product= "OTHER"
                               /note= "Xaa = hydrophobic amino acid,
                                     selected from Ala, Leu, Ile, Val, Pro,
                                     Phe, Trp or Met"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 10
      (D) OTHER INFORMATION: /product= "OTHER"
                               /note= "Xaa = hydrophobic amino acid,
                                       selected from Ala, Leu, Ile, Val, Pro,
                                       Phe, Trp or Met"
```

```
(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 11
      (D) OTHER INFORMATION: /product= "OTHER"
                               /note= "Xaa = hydrophobic amino acid,
                                     selected from Ala, Leu, Ile, Val, Pro,
                                     Phe, Trp or Met"
```

(ix) FEATURE:
(A) NAME/KEY: Modified-site

(B) LOCATION: 13
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid,
 selected from Gly, Ser, Thr, Tyr, Cys,
 Asn or Gln"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 21
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid,
 selected from Gly, Ser, Thr, Tyr, Cys,
 Asn or Gln"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 25
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = polar amino acid,
 selected from Gly, Ser, Thr, Tyr, Cys,
 Asn or Gln"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Trp	Leu	Xaa	Tyr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Phe	Tyr
1				5						10						15
Xaa	Thr	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Xaa	Arg	Lys
			20							25					30	
Xaa	Xaa	Trp														
		35														

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4038 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 56..3454
 (D) OTHER INFORMATION: /note= "refined hTRT DNA sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCAGCGCTGC	GTCCTGCTGC	GCACGTGGGA	AGCCCTGGCC	CCGGCCACCC	CCGCG	ATG	58
						Met	
						1	
CCG	CGC	GCT	CCC	CGC	TGC	CGA	GCC
Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala
			5				10
							15
							106

TAC	CGC	GAG	GTG	CTG	CCG	CTG	GCC	ACG	TTC	GTG	CGG	CGC	CTG	GGG	CCC	154
Tyr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	Pro	
		20					25						30			
CAG	GGC	TGG	CGG	CTG	GTG	CAG	CGC	GGG	GAC	CCG	GCG	GCT	TTC	CGC	GCG	202
Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	Ala	
	35					40					45					
CTG	GTG	GCC	CAG	TGC	CTG	GTG	TGC	GTG	CCC	TGG	GAC	GCA	CGG	CCG	CCC	250
Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	Pro	
	50				55					60					65	
CCC	GCC	GCC	CCC	TCC	TTC	CGC	CAG	GTG	TCC	TGC	CTG	AAG	GAG	CTG	GTG	298
Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu	Val	
				70					75					80		
GCC	CGA	GTG	CTG	CAG	AGG	CTG	TGC	GAG	CGC	GGC	GCG	AAG	AAC	GTG	CTG	346
Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	Leu	
			85					90					95			
GCC	TTC	GGC	TTC	GCG	CTG	CTG	GAC	GGG	GCC	CGC	GGG	GGC	CCC	CCC	GAG	394
Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	Glu	
		100					105					110				
GCC	TTC	ACC	ACC	AGC	GTG	CGC	AGC	TAC	CTG	CCC	AAC	ACG	GTG	ACC	GAC	442
Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	Asp	
	115					120					125					
GCA	CTG	CGG	GGG	AGC	GGG	GCG	TGG	GGG	CTG	CTG	CTG	CGC	CGC	GTG	GGC	490
Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	Gly	
	130				135					140					145	
GAC	GAC	GTG	CTG	GTT	CAC	CTG	CTG	GCA	CGC	TGC	GCG	CTC	TTT	GTG	CTG	538
Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	Leu	
				150					155					160		
GTG	GCT	CCC	AGC	TGC	GCC	TAC	CAG	GTG	TGC	GGG	CCG	CCG	CTG	TAC	CAG	586
Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	Gln	
			165					170						175		
CTC	GGC	GCT	GCC	ACT	CAG	GCC	CGG	CCC	CCG	CCA	CAC	GCT	AGT	GGA	CCC	634
Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	Pro	
		180					185					190				
CGA	AGG	CGT	CTG	GGA	TGC	GAA	CGG	GCC	TGG	AAC	CAT	AGC	GTC	AGG	GAG	682
Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	Glu	
	195					200					205					
GCC	GGG	GTC	CCC	CTG	GGC	CTG	CCA	GCC	CCG	GGT	GCG	AGG	AGG	CGC	GGG	730
Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	Gly	
	210				215					220					225	
GGC	AGT	GCC	AGC	CGA	AGT	CTG	CCG	TTG	CCC	AAG	AGG	CCC	AGG	CGT	GGC	778
Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	Gly	
				230				235						240		
GCT	GCC	CCT	GAG	CCG	GAG	CGG	ACG	CCC	GTT	GGG	CAG	GGG	TCC	TGG	GCC	826
Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	Ala	
			245					250						255		

CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG GTG	874
His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val	
260 265 270	
TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG GGT GCG CTC	922
Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu	
275 280 285	
TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC CAG CAC CAC GCG	970
Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala	
290 295 300 305	
GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC TGG GAC ACG CCT TGT	1018
Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys	
310 315 320	
CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC CTC TAC TCC TCA GGC GAC	1066
Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp	
325 330 335	
AAG GAG CAG CTG CGG CCC TCC TTC CTA CTC AGC TCT CTG AGG CCC AGC	1114
Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser	
340 345 350	
CTG ACT GGC GCT CGG AGG CTC GTG GAG ACC ATC TTT CTG GGT TCC AGG	1162
Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg	
355 360 365	
CCC TGG ATG CCA GGG ACT CCC CGC AGG TTG CCC CGC CTG CCC CAG CGC	1210
Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg	
370 375 380 385	
TAC TGG CAA ATG CGG CCC CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG	1258
Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala	
390 395 400	
CAG TGC CCC TAC GGG GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT	1306
Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala	
405 410 415	
GCG GTC ACC CCA GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC	1354
Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly	
420 425 430	
TCT GTG GCG GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG	1402
Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val	
435 440 445	
CAG CTG CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG	1450
Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val	
450 455 460 465	
CGG GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG	1498
Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg	
470 475 480	
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC CTG	1546
His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu	
485 490 495	

GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG ATG AGC Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser 500 505 510	1594
GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT GGC TGT GTT Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val 515 520 525	1642
CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG GCC AAG TTC CTG Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu 530 535 540 545	1690
CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG CTC AGG TCT TTC TTT His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe 550 555 560	1738
TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG CTC TTT TTC TAC CGG Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg 565 570 575	1786
CCG AGT GTC TGG AGC AAG TTG CAA AGC ATT GGA ATC AGA CAG CAC TTG Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu 580 585 590	1834
AAG AGG GTG CAG CTG CGG GAG CTG TCG GAA GCA GAG GTC AGG CAG CAT Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His 595 600 605	1882
CGG GAA GCC AGG CCC GCC CTG CTG ACG TCC AGA CTC CGC TTC ATC CCC Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro 610 615 620 625	1930
AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly 630 635 640	1978
GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg 645 650 655	2026
GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro 660 665 670	2074
GGC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala 675 680 685	2122
TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu 690 695 700 705	2170
CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro 710 715 720	2218
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn 725 730 735	2266

ACG	TAC	TGC	GTG	CGT	CGG	TAT	GCC	GTG	GTC	CAG	AAG	GCC	GCC	CAT	GGG	2314
Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	His	Gly	
		740					745					750				
CAC	GTC	CGC	AAG	GCC	TTC	AAG	AGC	CAC	GTC	TCT	ACC	TTG	ACA	GAC	CTC	2362
His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	Thr	Asp	Leu	
	755					760					765					
CAG	CCG	TAC	ATG	CGA	CAG	TTC	GTG	GCT	CAC	CTG	CAG	GAG	ACC	AGC	CCG	2410
Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	Thr	Ser	Pro	
770					775					780					785	
CTG	AGG	GAT	GCC	GTC	GTC	ATC	GAG	CAG	AGC	TCC	TCC	CTG	AAT	GAG	GCC	2458
Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	Asn	Glu	Ala	
				790					795					800		
AGC	AGT	GGC	CTC	TTC	GAC	GTC	TTC	CTA	CGC	TTC	ATG	TGC	CAC	CAC	GCC	2506
Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys	His	His	Ala	
			805					810					815			
GTG	CGC	ATC	AGG	GGC	AAG	TCC	TAC	GTC	CAG	TGC	CAG	GGG	ATC	CCG	CAG	2554
Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	Gln	
		820					825					830				
GGC	TCC	ATC	CTC	TCC	ACG	CTG	CTC	TGC	AGC	CTG	TGC	TAC	GGC	GAC	ATG	2602
Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	Met	
	835					840					845					
GAG	AAC	AAG	CTG	TTT	GCG	GGG	ATT	CGG	CGG	GAC	GGG	CTG	CTC	CTG	CGT	2650
Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg	
850					855					860					865	
TTG	GTG	GAT	GAT	TTC	TTG	TTG	GTG	ACA	CCT	CAC	CTC	ACC	CAC	GCG	AAA	2698
Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	Lys	
				870					875					880		
ACC	TTC	CTC	AGG	ACC	CTG	GTC	CGA	GGT	GTC	CCT	GAG	TAT	GGC	TGC	GTG	2746
Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	
			885					890					895			
GTG	AAC	TTG	CGG	AAG	ACA	GTG	GTG	AAC	TTC	CCT	GTA	GAA	GAC	GAG	GCC	2794
Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu	Asp	Glu	Ala	
		900					905					910				
CTG	GGT	GGC	ACG	GCT	TTT	GTT	CAG	ATG	CCG	GCC	CAC	GGC	CTA	TTC	CCC	2842
Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly	Leu	Phe	Pro	
	915					920					925					
TGG	TGC	GGC	CTG	CTG	CTG	GAT	ACC	CGG	ACC	CTG	GAG	GTG	CAG	AGC	GAC	2890
Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val	Gln	Ser	Asp	
930					935					940					945	
TAC	TCC	AGC	TAT	GCC	CGG	ACC	TCC	ATC	AGA	GCC	AGT	GTC	ACC	TTC	AAC	2938
Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala	Ser	Val	Thr	Phe	Asn	
				950					955					960		
CGC	GGC	TTC	AAG	GCT	GGG	AGG	AAC	ATG	CGT	CGC	AAA	CTC	TTT	GGG	GTC	2986
Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg	Lys	Leu	Phe	Gly	Val	
			965					970					975			

TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser 980 985 990	3034
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG GCG Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala 995 1000 1005	3082
TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG CAA GTT Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val 1010 1015 1020 1025	3130
TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC TCT GAC ACG GCC TCC Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser 1030 1035 1040	3178
CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC GCA GGG ATG TCG CTG GGG Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly 1045 1050 1055	3226
GCC AAG GGC GCC GCC GGC CCT CTG CCC TCC GAG GCC GTG CAG TGG CTG Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu 1060 1065 1070	3274
TGC CAC CAA GCA TTC CTG CTC AAG CTG ACT CGA CAC CGT GTC ACC TAC Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr 1075 1080 1085	3322
GTG CCA CTC CTG GGG TCA CTC AGG ACA GCC CAG ACG CAG CTG AGT CGG Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg 1090 1095 1100 1105	3370
AAG CTC CCG GGG ACG ACG CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro 1110 1115 1120	3418
GCA CTG CCC TCA GAC TTC AAG ACC ATC CTG GAC TGATGGCCAC CCGCCACAG Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp 1125 1130	3471
CCAGGCCGAG AGCAGACACC AGCAGCCCTG TCACGCCGGG CTCTACGTCC CAGGGAGGGA	3531
GGGGCGGCCC ACACCCAGGC CCGCACCGCT GGGAGTCTGA GGCCTGAGTG AGTGTTTGGC	3591
CGAGGCCTGC ATGTCCGGCT GAAGGCTGAG TGTCCGGCTG AGGCCTGAGC GAGTGTCCAG	3651
CCAAGGGCTG AGTGTCCAGC ACACCTGCCG TCTTCACTTC CCCACAGGCT GGCGCTCGGC	3711
TCCACCCAG GGCCAGCTTT TCYTACACAG GAGCCCGGCT TCCACTCCCC ACATAGGAAT	3771
AGTCCATCCC CAGATTCGCC ATTGTTACCC CYTCGCCCTG CCYTCCTTTG CCTTCCACCC	3831
CCACCATCCA GGTGGAGACC CTGAGAAGGA CCCTGGGAGC TCTGGGAATT TGGAGTGACC	3891
AAAGGTGTGC CCTGTACACA GGCGAGGACC CTGCACCTGG ATGGGGGTCC CTGTGGGTCA	3951
AATTGGGGGG AGGTGCTGTG GGAGTAAAT ACTGAATATA TGAGTTTTTC AGTTTTGRAA	4011
AAAAAAAAA AAAAAAAAAA AAAAAAA	4038

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815
 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
930 935 940

Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Val Thr Phe
945 950 955 960

Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
965 970 975

Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
980 985 990

Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
995 1000 1005

Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
1010 1015 1020

Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
1025 1030 1035 1040

Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
1045 1050 1055

Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
1060 1065 1070

Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
1075 1080 1085

Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
1090 1095 1100

Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
1105 1110 1115 1120

Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
1125 1130

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1 5 10 15

Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa
20 25 30

Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile
 35 40

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
 1 5 10 15
 Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa
 20 25 30
 Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile
 35 40

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Glu Xaa Xaa Val Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 56..2479
- (D) OTHER INFORMATION: /product= "hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC CCGCG ATG	58
Met	
1	
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC	106
Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His	
5 10 15	
TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC	154
Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro	
20 25 30	
CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG	202
Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala	
35 40 45	
CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC	250
Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro	
50 55 60 65	
CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG	298
Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val	
70 75 80	
GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG	346
Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu	
85 90 95	
GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG	394
Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu	
100 105 110	
GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC	442
Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp	
115 120 125	
GCA CTG CGG GGG AGC GGG GCG TGG GGG CTG CTG CTG CGC CGC GTG GGC	490
Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly	
130 135 140 145	
GAC GAC GTG CTG GTT CAC CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG	538
Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu	
150 155 160	
GTG GCT CCC AGC TGC GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG	586
Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln	
165 170 175	
CTC GGC GCT GCC ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC	634
Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro	
180 185 190	
CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG	682
Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu	
195 200 205	

GCC GGG GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly 210 215 220 225	730
GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly 230 235 240	778
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala 245 250 255	826
CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG GTG His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val 260 265 270	874
TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG GGT GCG CTC Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu 275 280 285	922
TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC CAG CAC CAC GCG Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala 290 295 300 305	970
GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC TGG GAC ACG CCT TGT Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys 310 315 320	1018
CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC CTC TAC TCC TCA GGC GAC Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp 325 330 335	1066
AAG GAG CAG CTG CGG CCC TCC TTC CTA CTC AGC TCT CTG AGG CCC AGC Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser 340 345 350	1114
CTG ACT GGC GCT CGG AGG CTC GTG GAG ACC ATC TTT CTG GGT TCC AGG Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg 355 360 365	1162
CCC TGG ATG CCA GGG ACT CCC CGC AGG TTG CCC CGC CTG CCC CAG CGC Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg 370 375 380 385	1210
TAC TGG CAA ATG CGG CCC CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala 390 395 400	1258
CAG TGC CCC TAC GGG GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala 405 410 415	1306
GCG GTC ACC CCA GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly 420 425 430	1354
TCT GTG GCG GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val 435 440 445	1402

CAG CTG CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val 450 455 460 465	1450
CGG GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg 470 475 480	1498
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC CTG His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu 485 490 495	1546
GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG ATG AGC Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser 500 505 510	1594
GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT GGC TGT GTT Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val 515 520 525	1642
CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG GCC AAG TTC CTG Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu 530 535 540 545	1690
CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG CTC AGG TCT TTC TTT His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe 550 555 560	1738
TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG CTC TTT TTC TAC CGG Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg 565 570 575	1786
AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT GGA ATC AGA CAG CAC TTG Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu 580 585 590	1834
AAG AGG GTG CAG CTG CGG GAG CTG TCG GAA GCA GAG GTC AGG CAG CAT Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His 595 600 605	1882
CGG GAA GCC AGG CCC GCC CTG CTG ACG TCC AGA CTC CGC TTC ATC CCC Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro 610 615 620 625	1930
AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly 630 635 640	1978
GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg 645 650 655	2026
GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro 660 665 670	2074
GGC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala 675 680 685	2122

TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG	2170
Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu	
690 695 700 705	
CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC	2218
Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro	
710 715 720	
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC	2266
Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn	
725 730 735	
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC CAT GGG	2314
Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly	
740 745 750	
CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA GTG CCA GGG	2362
His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro Gly	
755 760 765	
GAT CCC GCA GGG CTC CAT CCT CTC CAC GCT GCT CTG CAG CCT GTG CTA	2410
Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu	
770 775 780 785	
CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT TCG GCG GGA CGG GCT	2458
Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala	
790 795 800	
GCT CCT GCG TTT GGT GGA TGATTTCTTG TTGGTGACAC CTCACCTCAC	2506
Ala Pro Ala Phe Gly Gly	
805	
CCACGCGAAA ACCTTCCTCA GGACCCTGGT CCGAGGTGTC CCTGAGTATG GCTGCGTGGT	2566
GAACCTGCGG AAGACAGTGG TGAACCTCCC TGTAGAAGAC GAGGCCCTGG GTGGCACGGC	2626
TTTTGTTCAG ATGCCGGCCC ACGGCCTATT CCCCTGGTGC GGCCTGCTGC TGGATACCCG	2686
GACCCTGGAG GTGCAGAGCG ACTACTCCAG CTATGCCCCG ACCTCCATCA GAGCCAGTCT	2746
CACCTTCAAC CGCGGCTTCA AGGCTGGGAG GAACATGCGT CGCAAACCTCT TTGGGGTCTT	2806
GCGGCTGAAG TGTCACAGCC TGTTTCTGGA TTTGCAGGTG AACAGCCTCC AGACGGTGTG	2866
CACCAACATC TACAAGATCC TCCTGCTGCA GGCGTACAGG TTTCACGCAT GTGTGCTGCA	2926
GCTCCCATTT CATCAGCAAG TTTGGAAGAA CCCACATTT TTCCTGCGCG TCATCTCTGA	2986
CACGGCCTCC CTCTGCTACT CCATCCTGAA AGCCAAGAAC GCAGGGATGT CGCTGGGGGC	3046
CAAGGGCGCC GCCGGCCCTC TGCCCTCCGA GGCCGTGCAG TGGCTGTGCC ACCAAGCATT	3106
CCTGCTCAAG CTGACTCGAC ACCGTGTCAC CTACGTGCCA CTCCTGGGGT CACTCAGGAC	3166
AGCCCAGACG CAGCTGAGTC GGAAGCTCCC GGGGACGACG CTGACTGCCC TGGAGGCCGC	3226
AGCCAACCCG GCACTGCCCT CAGACTTCAA GACCATCCTG GACTGATGGC CACCCGCCCA	3286
CAGCCAGGCC GAGAGCAGAC ACCAGCAGCC CTGTCACGCC GGGCTCTACG TCCCAGGGAG	3346
GGAGGGGCGG CCCACACCCA GGCCCGCACC GCTGGGAGTC TGAGGCCTGA GTGAGTGTTT	3406

GGCCGAGGCC TGCATGTCCG GCTGAAGGCT GAGTGTCCGG CTGAGGCCTG AGCGAGTGTC 3466
 CAGCCAAGGG CTGAGTGTCC AGCACACCTG CCGTCTTCAC TTCCCCACAG GCTGGCGCTC 3526
 GGCTCCACCC CAGGGCCAGC TTTTCCTCAC CAGGAGCCCG GCTTCCACTC CCCACATAGG 3586
 AATAGTCCAT CCCCAGATTC GCCATTGTTC ACCCCTCGCC CTGCCCTCCT TTGCCTTCCA 3646
 CCCCCACCAT CCAGGTGGAG ACCCTGAGAA GGACCCTGGG AGCTCTGGGA ATTTGGAGTG 3706
 ACCAAAGGTG TGCCCTGTAC ACAGGCGAGG ACCCTGCACC TGGATGGGGG TCCCTGTGGG 3766
 TCAAATTGGG GGGAGGTGCT GTGGGAGTAA AATACTGAAT ATATGAGTTT TTCAGTTTTG 3826
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3855

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15
 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro
 755 760 765
 Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val
 770 775 780
 Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg
 785 790 795 800
 Ala Ala Pro Ala Phe Gly Gly
 805

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3025 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3025
- (D) OTHER INFORMATION: /note= "mouse TRT cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

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CGGGTGGGAG GCCCATCCCG GCCTTGAGCA CAATGACCCG CGCTCCTCGT TGCCCCGCGG      60
TGCGCTCTCT GCTGCGCAGC CGATACCGGG AGGTGTGGCC GCTGGCAACC TTTGTGCGGC      120
GCCTGGGGCC CGAGGGCAGG CGGCTTGTC AACCCGGGGA CCCGAAGATC TACCGCACTT      180
TGGTTGCCCA ATGCCTAGTG TGCATGCACT GGGGCTCACA GCCTCCACCT GCCGACCTTT      240
CCTTCCACCA GGTGTCATCC CTGAAAGAGC TGGTGGCCAG GGTTGTGCAG AGACTCTGCG      300
AGCGCAACGA GAGAAACGTG CTGGCTTTTG GCTTTGAGCT GCTTAACGAG GCCAGAGGCG      360
GGCCTCCCAT GGCCTTCACT AGTAGCGTGC GTAGCTACTT GCCCAACACT GTTATTGAGA      420
CCCTGCGTGT CAGTGGTGCA TGGATGCTAC TGTTGAGCCG AGTGGGCGAC GACCTGCTGG      480
TCTACCTGCT GGCACACTGT GCTCTTTATC TTCTGGTGCC CCCCAGCTGT GCCTACCAGG      540
TGTGTGGGTC TCCCCTGTAC CAAATTTGTG CCACCACGGA TATCTGGCCC TCTGTGTCCG      600
CTAGTTACAG GCCCACCCGA CCCGTGGGCA GGAATTTTAC TAACCTTAGG TTCTTACAAC      660
AGATCAAGAG CAGTAGTCGC CAGGAAGCAC CGAAACCCCT GGCCTTGCCA TCTCGAGGTA      720
CAAAGAGGCA TCTGAGTCTC ACCAGTACAA GTGTGCCTTC AGCTAAGAAG GCCAGATGCT      780
ATCCTGTCCC GAGAGTGGAG GAGGGACCCC ACAGGCAGGT GCTACCAACC CCATCAGGCA      840
AATCATGGGT GCCAAGTCCT GCTCGGTCCC CCGAGGTGCC TACTGCAGAG AAAGATTTGT      900
CTTCTAAAGG AAAGGTGTCT GACCTGAGTC TCTCTGGGTC GGTGTGCTGT AAACACAAGC      960
CCAGCTCCAC ATCTCTGCTG TCACCACCCC GCCAAAATGC CTTTCAGCTC AGGCCATTTA     1020
TTGAGACCAG ACATTTCTTT TACTCCAGGG GAGATGGCCA AGAGCGTCTA AACCCTCAT      1080
TCCTACTCAG CAACCTCCAG CCTAACTTGA CTGGGGCCAG GAGACTGGTG GAGATCATCT      1140
TTCTGGGCTC AAGGCCTAGG ACATCAGGAC CACTCTGCAG GACACACCGT CTATCGCGTC      1200
GATACTGGCA GATGCGGCCC CTGTTCCAAC AGCTGCTGGT GAACCATGCA GAGTGCCAAT      1260

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ATGTCAGACT	CCTCAGGTCA	CATTGCAGGT	TTCGAACAGC	AAACCAACAG	GTGACAGATG	1320
CCTTGAACAC	CAGCCCACCG	CACCTCATGG	ATTTGCTCCG	CCTGCACAGC	AGTCCCCTGGC	1380
AGGTATATGG	TTTTCTTCGG	GCCTGTCTCT	GCAAGGTGGT	GTCTGCTAGT	CTCTGGGGTA	1440
CCAGGCACAA	TGAGCGCCGC	TTCTTTAAGA	ACTTAAAGAA	GTTTCATCTCG	TTGGGGAAAT	1500
ACGGCAAGCT	ATCACTGCAG	GAAGTATGT	GGAAGATGAA	AGTAGAGGAT	TGCCACTGGC	1560
TCCGCAGCAG	CCCGGGGAAG	GACCGTGTCC	CCGCTGCAGA	GCACCGTCTG	AGGGAGAGGA	1620
TCCTGGCTAC	GTTCTGTTC	TGGCTGATGG	ACACATACGT	GGTACAGCTG	CTTAGGTCAT	1680
TCTTTTACAT	CACAGAGAGC	ACATTCCAGA	AGAACAGGCT	CTTCTTCTAC	CGTAAGAGTG	1740
TGTGGAGCAA	GCTGCAGAGC	ATTGGAGTCA	GGCAACACCT	TGAGAGAGTG	CGGCTACGGG	1800
AGCTGTCACA	AGAGGAGGTC	AGGCATCACC	AGGACACCTG	GCTAGCCATG	CCCATCTGCA	1860
GACTGCGCTT	CATCCCCAAG	CCCAACGGCC	TGCGGCCCAT	TGTGAACATG	AGTTATAGCA	1920
TGGGTACCAG	AGCTTTGGGC	AGAAGGAAGC	AGGCCAGCA	TTTCACCCAG	CGTCTCAAGA	1980
CTCTCTTCAG	CATGCTCAAC	TATGAGCCGA	CAAAACATCC	TCACCTTATG	GGGTCTTCTG	2040
TACTGGGTAT	GAATGACATC	TACAGGACCT	GGCGGGCCTT	TGTGCTGCGT	GTGCGTGCTC	2100
TGGACCANAC	ACCANGATGT	ACTTTGTAA	GGCAGATGTG	ACCGGGGCCT	ATGATGCCAT	2160
CCCCAGGGTA	AGCTGGGTGN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	2220
TGGTGGAGGT	TGTTGCCAAT	ATGATCAGGC	ATTCCGAGAG	CACGTACTGT	ATCCGCCAGT	2280
ATGCAGTGGT	CCGGAGAGAT	AGCCAAGGCC	AAGTCCACAA	GTCNTTTAGG	AGACAGGTCA	2340
CCACCTTCTC	TGACTTCCAG	CCATACATGG	GCCAGTTCCT	TAAGCATCTG	CAGGATTCAG	2400
ATGCCAGTGC	ACTGAGGAAC	TCCGTTGTCA	TGCAGCAGAG	CATCTCTATG	AATGAGAGCA	2460
GCAGCAGCCT	GTTTGATTCT	TCCTGCACTT	CCTGCGTCAC	AGTGTCGTAA	AGATTGGTGA	2520
CAGGTGCTAT	ACGCAGTGCC	AGGGCATCCC	CCAGGGCTCC	AGCCTATCCA	CCCTGCTCTG	2580
CAGTCTGTGT	TTCGGAGACA	TGGAGAACAA	GCTGTTTGCT	GAGGTGCAGC	GGGATGGGTT	2640
GCTTTTACGT	TTTGTTGATG	ACTTTCTGTT	GGTGACGCCT	CACTTGACC	AAGCANNNNN	2700
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	2760
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	2820
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	2880
NNNNNNNNNN	CTGCAGTTAT	GCCCAGACCT	CAATTAAGAC	GAGCCTCACC	TTCCAGAGTG	2940
TCTTCAAAGC	TGGGAAGACC	ATGCGGAACA	AGCTCCTGTC	GGTCTTGCGG	TTGAAGTGTC	3000
ACGGTCTATT	TCTAGACTTG	CAGGT				3025

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CTTTTACATC ACAGAGAGCA C

21

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTCGGACCAG GGTCCCTGAGG AA

22

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Cys	Gly	Gly	Gln	Lys	Gln	Leu	Glu	Phe	Tyr	Phe	Ser	Asp	Ala	Asn	Leu
1				5				10						15	
Tyr Asn Asp Ser Phe Leu															
20															

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn
 1 5 10 15
 Glu Phe Arg Ile Ile
 20

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Cys Leu Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr
 1 5 10 15
 Asp Ser Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys
 20 25

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp
 1 5 10 15
 Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala His Trp
 20 25 30
 Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp
 35 40 45
 Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Arg Ile Asp His Asn
 50 55 60
 Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu
 65 70 75 80
 Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser
 85 90 95

Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
 100 105 110
 Ser Gly Asp Asp Asp Asp Lys Val Pro Met His Glu Leu Glu Ile Phe
 115 120 125
 Glu Phe Ala Ala Ala Ser Thr Gln Arg Cys Val Leu Leu Arg Thr Trp
 130 135 140
 Glu Ala Leu Ala Pro Ala Thr Pro Ala Met Pro Arg Ala Pro Arg Cys
 145 150 155 160
 Arg Ala Val Arg Ser Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro
 165 170 175
 Leu Ala Thr Phe Val Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val
 180 185 190
 Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu
 195 200 205
 Val Cys Val Pro Trp Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe
 210 215 220
 Arg Gln Val Ser Cys Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg
 225 230 235 240
 Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu
 245 250 255
 Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val
 260 265 270
 Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly
 275 280 285
 Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His
 290 295 300
 Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala
 305 310 315 320
 Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln
 325 330 335
 Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys
 340 345 350
 Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly
 355 360 365
 Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser
 370 375 380
 Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu
 385 390 395 400
 Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg
 405 410 415

Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala
 420 425 430
 Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser
 435 440 445
 His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser
 450 455 460
 Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu
 465 470 475 480
 Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro
 485 490 495
 Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg
 500 505 510
 Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr
 515 520 525
 Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro
 530 535 540
 Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val
 545 550 555 560
 Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala
 565 570 575
 Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu
 580 585 590
 Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His
 595 600 605
 Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg
 610 615 620
 Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe
 625 630 635 640
 Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu
 645 650 655
 Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp
 660 665 670
 Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg
 675 680 685
 Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val
 690 695 700
 Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
 705 710 715 720
 Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys
 725 730 735

Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg
 740 745 750
 Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala
 755 760 765
 Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg
 770 775 780
 Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg
 785 790 795 800
 Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser
 805 810 815
 Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser
 820 825 830
 Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu
 835 840 845
 Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val
 850 855 860
 Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu
 865 870 875 880
 Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg
 885 890 895
 Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe
 900 905 910
 Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln
 915 920 925
 Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val
 930 935 940
 Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp
 945 950 955 960
 Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
 965 970 975
 Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr
 980 985 990
 Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala
 995 1000 1005
 Gly Ile Arg Arg Asp Gly Leu Leu Arg Leu Val Asp Asp Phe Leu
 1010 1015 1020
 Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu
 1025 1030 1035 1040
 Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr
 1045 1050 1055

Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe
 1060 1065 1070
 Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
 1075 1080 1085
 Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg
 1090 1095 1100
 Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly
 1105 1110 1115 1120
 Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His
 1125 1130 1135
 Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr
 1140 1145 1150
 Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys
 1155 1160 1165
 Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe
 1170 1175 1180
 Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu
 1185 1190 1195 1200
 Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly
 1205 1210 1215
 Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu
 1220 1225 1230
 Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser
 1235 1240 1245
 Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr
 1250 1255 1260
 Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe
 1265 1270 1275 1280
 Lys Thr Ile Leu Asp
 1285

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Arg Arg Ala Ser Val Gly Ser Val Thr Lys Ile Pro Gln Gly
 225 230 235 240
 Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu
 245 250 255
 Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu
 260 265 270
 Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr
 275 280 285
 Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val
 290 295 300
 Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu
 305 310 315 320
 Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp
 325 330 335

Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr
 340 345 350
 Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Val Thr Phe Asn Arg
 355 360 365
 Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu
 370 375 380
 Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu
 385 390 395 400
 Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr
 405 410 415
 Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp
 420 425 430
 Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu
 435 440 445
 Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala
 450 455 460
 Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys
 465 470 475 480
 His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val
 485 490 495
 Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys
 500 505 510
 Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala
 515 520 525
 Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 530 535

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Arg Arg Ala Ser Val Gly Ser Val His His His His His His
 225 230 235 240
 His His Gly Ser Val Thr Lys Met Ser Val Tyr Val Val Glu Leu Leu
 245 250 255
 Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu
 260 265 270
 Phe Phe Tyr Arg Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile
 275 280 285
 Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu
 290 295 300
 Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu
 305 310 315 320
 Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp
 325 330 335
 Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg
 340 345 350
 Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg
 355 360 365

Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp
 370 375 380

Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp
 385 390 395 400

Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr
 405 410 415

Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile
 420 425 430

Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys
 435 440 445

Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr
 450 455 460

Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln
 465 470 475 480

Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser
 485 490 495

Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met
 500 505 510

Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln
 515 520 525

Gly Ile
 530

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu
 20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Arg Arg Ala Ser Val Gly Ser Val Thr Lys Met Ser Val Tyr
 225 230 235 240
 Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe
 245 250 255
 Gln Lys Asn Arg Leu Phe Phe Tyr Arg Pro Ser Val Trp Ser Lys Leu
 260 265 270
 Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu
 275 280 285
 Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu
 290 295 300
 Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro
 305 310 315 320
 Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu
 325 330 335
 Lys Arg Ala Glu Arg Leu Thr Ser Arg Lys Ala Leu Phe Ser Val Leu
 340 345 350
 Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu
 355 360 365
 Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val
 370 375 380
 Arg Ala Gln Asp Pro Pro Pro Glu Tyr Phe Val Lys Val Asp Val Thr
 385 390 395 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
1				5					10					15	
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu
			20					25					30		
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
		35					40					45			
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
	50					55					60				
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
65					70					75					80
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
				85					90					95	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
			100					105					110		
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu
		115					120					125			

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Arg Arg Ala Ser Val Gly Ser Val Thr Lys Ala Thr Ser Leu
 225 230 235 240
 Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg
 245 250 255
 Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp
 260 265 270
 Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr
 275 280 285
 Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser
 290 295 300
 Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe
 305 310 315 320
 Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg
 325 330 335
 Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu
 340 345 350
 Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys
 355 360 365
 Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu
 370 375 380
 Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro
 385 390 395 400
 Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val
 405 410 415
 Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu
 420 425 430
 Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys
 435 440 445

Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr
 450 455 460
 Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly
 465 470 475 480
 Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu
 485 490 495
 Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
 500 505 510
 Arg Ser

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	180	185	190
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	195	200	205
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	210	215	220
Gly	Ser	Arg	Arg	Ala	Ser	Val	Gly	Ser	Val	Thr	Lys	Met	Pro	Arg	Ala	225	230	235
Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	Leu	Leu	Ser	His	Tyr	Arg	Glu	Val	245	250	255
Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	Pro	Gln	Gly	Trp	Arg	260	265	270
Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	Ala	Leu	Val	Ala	Gln	275	280	285
Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	Pro	Ala	Ala	Pro	Ser	290	295	300
Phe	Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	305	310	315
Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	325	330	335
Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	Glu	Ala	Thr	Thr	Ser	Val	340	345	350
Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	355	360	365
Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	370	375	380
Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	Leu	Val	Ala	Pro	Cys	Ala	Tyr	385	390	395
Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	405	410	415
Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	420	425	430
Arg	Ala	Trp	Asn	His	Ser	Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	435	440	445
Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	450	455	460
Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	465	470	475
Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	485	490	495

Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu
 500 505 510

Glu Ala Thr Ser Leu
 515

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CCGGCCACCC CCCATATGCC GCGCGCTCCC

30

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

TGCGCACGTG GGAAGCCCTG GCAGATCTGA ATTCCACCAT GCCGCGCGCT CCCCCTG

58

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGGGACGGGC TGCTCCTGCG TTTGGTGGAC GCGTTCTTGT TGGTGACACC TCACCTCACC

60

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Xaa	Xaa	Xaa	Arg	Xaa	Xaa	Pro	Lys	Xaa	Xaa	Xaa
1				5					10	

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met	Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser
1				5					10					15	
His	Tyr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly
			20					25					30		
Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg
		35					40					45			
Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro
	50					55				60					
Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu
65					70					75				80	
Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val
			85						90					95	
Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro
			100					105					110		
Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr
			115				120					125			
Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val
	130					135					140				
Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val
145					150					155				160	
Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr
			165						170					175	
Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly
			180					185					190		

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815
 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910
 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925
 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
 945 950 955 960
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
 995 1000 1005
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020
 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040
 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
 1045 1050 1055
 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
 1060 1065 1070
 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
 1075 1080 1085
 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
 1090 1095 1100
 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
 1105 1110 1115 1120
 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp Leu Glu Gln Lys
 1125 1130 1135
 Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His
 1140 1145 1150
 His His

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```

Met Pro Arg Gly Ser His His His His His His Gly Met Ala Ser Met
1           5           10           15

Thr Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Leu
          20           25           30

Asp Pro Ser Ser Arg Ser Ala Ala Gly Thr Met Glu Phe Ala Ala Ala
          35           40           45

Ser Thr Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro
          50           55           60

Ala Thr Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser
          65           70           75           80

Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val
          85           90           95

Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro
          100          105          110

Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp
          115          120          125

Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys
          130          135          140

Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly
          145          150          155          160

Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg
          165          170          175

Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro
          180          185          190

Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu
          195          200          205

Leu Arg Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys
          210          215          220

Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly
          225          230          235          240

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Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro
 245 250 255
 His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn
 260 265 270
 His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly
 275 280 285
 Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys
 290 295 300
 Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly
 305 310 315 320
 Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg
 325 330 335
 Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser
 340 345 350
 Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly
 355 360 365
 Arg Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro
 370 375 380
 Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu
 385 390 395 400
 Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser
 405 410 415
 Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile
 420 425 430
 Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro
 435 440 445
 Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu
 450 455 460
 Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His
 465 470 475 480
 Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg
 485 490 495
 Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp
 500 505 510
 Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln
 515 520 525
 Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly
 530 535 540
 Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys
 545 550 555 560

Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu
 565 570 575
 Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro
 580 585 590
 Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile
 595 600 605
 Leu Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu
 610 615 620
 Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg
 625 630 635 640
 Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
 645 650 655
 Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala
 660 665 670
 Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg
 675 680 685
 Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met
 690 695 700
 Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu
 705 710 715 720
 Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu
 725 730 735
 Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp
 740 745 750
 Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln
 755 760 765
 Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala
 770 775 780
 Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
 785 790 795 800
 Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
 805 810 815
 Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
 820 825 830
 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
 835 840 845
 Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
 850 855 860
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 865 870 875 880

Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 885 890 895
 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
 900 905 910
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
 915 920 925
 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
 930 935 940
 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
 945 950 955 960
 Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
 965 970 975
 Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
 980 985 990
 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
 995 1000 1005
 Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
 1010 1015 1020
 Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
 1025 1030 1035 1040
 Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
 1045 1050 1055
 Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
 1060 1065 1070
 Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
 1075 1080 1085
 Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
 1090 1095 1100
 Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala
 1105 1110 1115 1120
 Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu
 1125 1130 1135
 Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg
 1140 1145 1150
 His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln
 1155 1160 1165
 Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu
 1170 1175 1180
 Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1185 1190 1195 1200

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```

Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
1           5           10           15

Ser Tyr Ile Tyr Ala Asp Pro Ser Ser Arg Ser Ala Ala Gly Thr Met
          20           25           30

Glu Phe Ala Ala Ala Ser Thr Gln Arg Cys Val Leu Leu Arg Thr Trp
          35           40           45

Glu Ala Leu Ala Pro Ala Thr Pro Ala Met Pro Arg Ala Pro Arg Cys
          50           55           60

Arg Ala Val Arg Ser Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro
65           70           75           80

Leu Ala Thr Phe Val Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val
          85           90           95

Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu
          100          105          110

Val Cys Val Pro Trp Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe
          115          120          125

Arg Gln Val Ser Cys Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg
          130          135          140

Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu
145          150          155          160

Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val
          165          170          175

Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly
          180          185          190

Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His
          195          200          205

Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala
          210          215          220

Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln
225          230          235          240

Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys
          245          250          255

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Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly
 260 265 270
 Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser
 275 280 285
 Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu
 290 295 300
 Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg
 305 310 315 320
 Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala
 325 330 335
 Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser
 340 345 350
 His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser
 355 360 365
 Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu
 370 375 380
 Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro
 385 390 395 400
 Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg
 405 410 415
 Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr
 420 425 430
 Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro
 435 440 445
 Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val
 450 455 460
 Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala
 465 470 475 480
 Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu
 485 490 495
 Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His
 500 505 510
 Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg
 515 520 525
 Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe
 530 535 540
 Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu
 545 550 555 560
 Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp
 565 570 575

Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg
 580 585 590
 Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val
 595 600 605
 Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
 610 615 620
 Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys
 625 630 635 640
 Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg
 645 650 655
 Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala
 660 665 670
 Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg
 675 680 685
 Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg
 690 695 700
 Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser
 705 710 715 720
 Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser
 725 730 735
 Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu
 740 745 750
 Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val
 755 760 765
 Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu
 770 775 780
 Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg
 785 790 795 800
 Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe
 805 810 815
 Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln
 820 825 830
 Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val
 835 840 845
 Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp
 850 855 860
 Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
 865 870 875 880
 Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr
 885 890 895

Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala
 900 905 910
 Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu
 915 920 925
 Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu
 930 935 940
 Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr
 945 950 955 960
 Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe
 965 970 975
 Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
 980 985 990
 Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg
 995 1000 1005
 Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly
 1010 1015 1020
 Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His
 1025 1030 1035 1040
 Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr
 1045 1050 1055
 Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys
 1060 1065 1070
 Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe
 1075 1080 1085
 Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu
 1090 1095 1100
 Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly
 1105 1110 1115 1120
 Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu
 1125 1130 1135
 Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser
 1140 1145 1150
 Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr
 1155 1160 1165
 Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe
 1170 1175 1180
 Lys Thr Ile Leu Asp
 1185

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Xaa Arg Xaa Ile Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Tyr Asp Xaa
1 5 10 15
Xaa

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CTGCCCTCAG ACTTCAAGAC CATCCTGGAC TACAAGGACG ACGATGACAA ATGAATTCAG 60
ATCTGCGGCC GCCACCGCGG TGGAGCTCCA GC 92

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Tyr Xaa Xaa Xaa Xaa Gly Xaa Xaa Gln Gly Xaa Xaa Xaa Ser Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa
 20

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Xaa Xaa Xaa Xaa Xaa Xaa Asp Asp Xaa Leu Xaa Xaa Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TTYTTYTAYG TNACNGA

17

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TCNGTNACRT ARAARAA

17

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

MGNTTYATHC CNAARCC

17

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GCCACCCCCG CGCTGCCTCG AGCTCCCCGC TGC

33

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Pro	Gln	Asn	Pro	Lys	Thr	Pro	Lys	Pro	Leu
1				5					10

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Lys Lys Lys Lys Leu Arg
1 5

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Phe Arg Asn Lys Ile Leu Phe Pro His Lys Trp Arg Trp Ile Leu Ile
1 5 10 15
Trp Met Ile

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Lys Ile Tyr Phe Leu Ile His Ser Thr Ser Ile Ala Ala Leu Val Val
1 5 10 15
Thr Arg Lys Asp Ala Lys His Cys Asn Leu Ala Arg Asn Arg Leu His
20 25 30
Cys Leu Phe Gln Ser Cys Lys Asn Asn
35 40

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Ser Ser Thr Ser Arg Met Gln Ile Phe Ile Thr Ile Leu Ser Cys Glu
1 5 10 15

Asn

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Lys Ala Glu Ser Lys Glu
1 5

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Lys Leu Lys His Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Cys Leu Asn Lys Ile Arg
1 5

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Cys	Gly	Leu	Phe	Tyr	Phe	Leu	Asp	His	Phe	Leu	Arg	Ser	Ile	Met	Glu
1				5					10					15	
Lys Ile Thr															

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Lys	Val	Asn	Ser	Leu	Asp	Tyr	Phe	Pro	Ser	Gln	Gln	Cys	Cys	Val	Tyr
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Ile	His	Met	Arg	Met	Ser	Gln	Arg	Ile	Ser	Ile	His	Gln	Thr	Tyr	Gln
1				5					10					15	
Arg Gln Thr Arg Tyr Lys Thr Gln Glu Lys Val Cys															
				20					25						

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Ser	Asn	Ser	Arg	Arg	Thr	Tyr	Cys	Ile	Tyr	Tyr	Ser	Tyr	Gly	Phe	Tyr
1				5					10					15	
Tyr	Asn	Cys	Phe	Arg	Tyr	Arg	Arg	Cys	Thr	Pro	Glu	Ser	Cys	Asp	Asn
			20					25					30		
Cys	Lys	Ser	Cys	Leu	Gln	Leu	Lys	Glu	Ser	Gln	Phe	Cys	Lys	Phe	Cys
		35					40					45			
Cys	Val	Cys	His	Tyr	Phe	Val	Asn								
	50					55									

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

[illegible]

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Phe	Phe	Ile	Ser	Gln	Leu	Leu	Phe	Ser	Phe	Ile	Leu	Thr	Ile	Phe	Phe
1				5				10						15	

Asp

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Leu	Glu	Val	Lys	Ser	Ile	Lys
1				5		

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Thr	Glu	Val	Thr
1			

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Leu Ile His Ile His Arg Ser Thr Phe Ile Tyr Pro Ile Arg Cys
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Gly Asn Ser Ser His Pro Phe
 1 5

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Cys Tyr Glu Asp
 1

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Ile Phe Arg Val Lys Lys Trp Ser Arg Asn Leu Asn Gln Lys Glu Leu
 1 5 10 15
 Arg Arg Tyr Cys Lys Arg Ile Glu Leu
 20 25

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Val	Leu	Pro	Ile	Leu	Ile	Asp	Cys	Arg	Asp	Cys	Arg	Gly	Asn	Cys	Thr
1				5				10						15	
Glu Asp His															

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Arg	Asn	Lys	Val	Thr	Phe	Ile	Asn
1				5			

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ile	Thr	Asn	Ile	Glu	Ile	Ser	Asp	Leu	Gln	Leu	Thr	Lys
1				5				10				

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Thr Ile Lys Asn Thr Asn Leu Gly Gln Asn Ile Glu Glu Gly Lys Glu
1 5 10 15

Asp Gln Leu Ala Lys Glu Lys Ile Arg Gln
20 25

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Ile Lys Cys Val Gln Lys Cys Arg Asn Lys Arg Phe Ile Phe Phe Asn
1 5 10 15

Asn Leu Leu Lys Arg Gly Val Leu Gly Phe Trp Gly Phe Gly
20 25 30

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Pro	Lys	Thr	Pro	Lys	Pro	Gln	Asn	Pro	Tyr	Lys	Lys	Arg	Lys	Asn	Cys
1				5					10					15	
Gly	Ser	Leu	Glu	Ile	Lys	Tyr	Tyr	Ser	Arg	Thr	Asn	Gly	Asp	Gly	Tyr
			20					25					30		
Cys	Phe	Gly	Cys	Tyr	Arg	Lys	Phe	Thr	Ser						
		35					40								

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Tyr Ile Gln Gln Val
1 5

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Cys Gln Glu Arg Met Gln Asn Ile Glu Ile Trp Leu Glu Ile Ala Phe
1 5 10 15
Ile Asp Tyr Ser Lys Val Ala Lys Thr Ile Arg Val Leu Leu Leu Gly
20 25 30
Cys Lys Ser Leu
35

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Arg Phe Phe Leu Glu Lys Ile Ser Phe Lys Lys Arg Arg Ala Lys Ser
1 5 10 15
Arg Asn Cys Asn Ile Thr Asn Val
20

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Ile	Lys	Ser	Gly	Asn	Glu	Asp	Tyr	Ser	Ile	Phe
1				5					10	

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Gly	Ala	Leu	Trp	Arg	Lys	Leu	Leu	Asn	Thr	Lys	Arg
1				5					10		

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Thr	Val	Trp	Ile	Ile	Ser	Leu	Ala	Asn	Asn	Asp	Glu	Tyr	Ile	Lys	Phe
1				5					10					15	
Ile	Cys	Glu	Cys	Val	Lys	Gly	Ser	Arg	Tyr	Ile	Arg	Leu	Thr	Lys	Asp
			20					25					30		
Lys	Leu	Ala	Ile	Lys	Arg	Lys	Lys	Lys	Phe	Asp	Asn	Arg	Thr	Ala	Glu
		35					40					45			
Glu	Leu	Ile	Ala	Phe	Thr	Ile	Arg	Met	Gly	Phe	Ile	Thr	Ile	Val	Leu
	50					55					60				
Gly	Ile	Asp	Gly	Glu	Leu	Pro	Ser	Leu	Glu	Thr	Ile	Glu	Lys	Ala	Val
65					70					75				80	
Tyr	Asn	Cys	Arg	Asn	Arg	Ser	Ser	Glu	Ser	Ser	Asp	Val	Tyr	Ala	Ile
				85					90					95	
Ile	Leu	Cys	Ile	Asn	Leu	Lys	Tyr	Leu	Ile	Ser	Ile				
			100					105							

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Trp Ile Ala Ile Glu Thr Asn Gln Ile Asn His Ala Ser Leu Met Glu
 1 5 10 15

Tyr Thr Leu Asn Pro Leu Gly Gln Met His Thr Glu Phe Ile Leu Asp
 20 25 30

Ser

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Ser Ile Asp Thr Gln Asn Ala Leu Glu Thr Asp Leu Ala Tyr Asn Arg
 1 5 10 15

Leu Pro Val Leu Ile Thr Leu Ala His Leu Leu Tyr Leu
 20 25

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Lys Lys Gln Ala Lys Cys Lys Glu Asp
 1 5

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Arg Lys Arg Phe Gln Asn Leu Leu Ile Leu Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Pro Glu Leu Thr Thr Arg Ile Leu Ala Thr Lys Lys Lys Lys Ser Tyr
 1 5 10 15

His Asn Pro Asp Ser
 20

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Arg Phe Gln Lys Phe Gln Val Arg Glu Ile His Ser Leu Lys Phe Ile
 1 5 10 15

Tyr Tyr Ser Phe Ser Phe His Ser Cys Tyr Phe Leu Leu Ser
 20 25 30

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Gln Tyr Phe Leu Ile Ser Trp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Lys Val Ser Asn Lys Arg Ser Ala Arg Leu Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Leu Ser Leu Phe Thr Phe Ile Asp Arg Pro Ser Tyr Ile Gln Tyr Asp
1 5 10 15

Asp Lys Glu Thr Ala Val Ile Arg Phe Lys Asn Ser Ala Met Arg Thr
20 25 30

Lys Phe Leu Glu Ser Arg Asn Gly Ala Glu Ile Leu Ile Lys Lys Asn
35 40 45

Cys Val Asp Ile Ala Lys Glu Ser Asn Ser Lys Ser Phe Val Asn Lys
50 55 60

Tyr Tyr Gln Ser Cys Leu Ile Glu Glu Ile Asp Glu Ala Thr Ala Gln
65 70 75 80

Lys Ile Ile Lys Glu Ile Lys
85

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Leu Leu Leu Ile Arg Glu
1 5

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Thr Lys Leu Leu Ile
1 5

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Arg Ser Ala Ile Phe Asn Cys Arg Asn Lys Ser Cys Thr Lys Val Arg
1 5 10 15
Gln

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Lys	Ile	Gln	Thr	Leu	Val	Lys	Ile	Leu	Arg	Lys	Glu	Lys	Lys	Thr	Ser
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Gln	Lys	Lys	Lys
1			

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Asn	Glu	Tyr	Arg	Ser	Glu	Glu	Ile	Lys	Asp	Leu	Phe	Phe	Ser	Ile	Ile
1				5				10						15	
Tyr	Cys	Lys	Glu	Gly	Phe	Trp	Gly	Phe	Gly	Val	Leu	Gly			
										20			25		

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Pro	Lys	Pro	Gln	Asn	Pro	Lys	Thr	Pro	Ile	Lys	Lys	Glu	Lys	Ile	Glu
1				5				10						15	
Val	Val														

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Asn Ile Ile Pro Ala Gln Met Glu Met Asp Ile Asp Leu Asp Asp Ile
 1 5 10 15

Glu Asn Leu Leu Pro Asn Thr Phe Asn Lys Tyr Ser Ser Ser Cys Ser
 20 25 30

Asp Lys Lys Gly Cys Lys Thr Leu Lys Ser Gly Ser Lys Ser Pro Ser
 35 40 45

Leu Thr Ile Pro Lys Leu Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp
 50 55 60

Ala Asn Leu Tyr Asn Asp Ser Phe Leu Arg Lys Leu Val Leu Lys Ser
 65 70 75 80

Gly Glu Gln Arg Val Glu Ile Glu Thr Leu Leu Met Phe Lys
 85 90

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Asn Gln Val Met Arg Ile Ile Leu Phe Phe Arg Ser Leu Leu Lys Glu
 1 5 10 15

His Tyr Gly Glu Asn Tyr Leu Ile Leu Lys Gly Lys Gln Phe Gly Leu
 20 25 30

Phe Pro

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Pro	Thr	Met	Met	Ser	Ile	Leu	Asn	Ser	Tyr	Glu	Asn	Glu	Ser	Lys	Asp
1				5					10					15	
Leu	Asp	Thr	Ser	Asp	Leu	Pro	Lys	Thr	Asn	Ser	Leu				
				20				25							

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Asn	Ala	Arg	Lys	Ser	Leu	Ile	Ile	Glu	Gln	Gln	Lys	Asn	Leu	Leu	His
1				5				10						15	
Leu	Leu	Phe	Val	Trp	Val	Leu	Leu	Gln	Leu	Phe					
				20				25							

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Val	Ser	Thr	Val	Asn	Ser	Arg	Val	Leu	Arg	Gln	Leu	Lys	Lys	Leu	Phe
1				5				10						15	
Thr	Thr	Glu	Gly	Ile	Ala	Val	Leu	Lys	Val	Leu	Met	Cys	Met	Pro	Leu
			20				25					30			
Phe	Cys	Glu	Leu	Ile	Ser	Asn	Ile	Leu	Ser	Gln	Phe	Asn	Gly		
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Lys Gln Thr Lys
1

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Thr Met Gln Val
1

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Trp Asn Ile Arg
1

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Ile Leu Trp Asp Lys Cys Thr Leu Asn Leu Tyr Trp Ile Leu Lys Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Ile His Arg Met Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Leu Thr Thr Asp Tyr Leu Phe Cys Leu Leu Leu Ile Ser Tyr Ile
 1 5 10 15

Phe Lys Arg Ser Arg Arg Asn Glu Lys Lys Thr Lys Glu Arg Asp Phe
 20 25 30

Lys Ile Cys Cys Phe Phe Cys Asn Arg Asn
 35 40

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Gln Gln Glu Tyr
 1

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Gln Arg Lys Arg Arg Arg Ala Ile Thr Ile Leu Ile Leu Lys Asp Phe
1 5 10 15
Lys Asn Ser Arg
20

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Glu Arg Tyr Ile His
1 5

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Asn	Ser	Tyr	Ile	Ile	Val	Phe	His	Phe	Thr	Ala	Val	Ile	Phe	Phe	Tyr
1				5					10					15	
Leu	Asn	Asn	Ile	Phe	Cys	Leu	Ala	Gly	Ser	Lys	Lys	Tyr	Gln	Ile	Arg
			20					25					30		
Glu	Ala	Leu	Asp	Cys	Gly	Asn	Leu	Ala	Tyr	Ser	His	Ser			
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```

Ile Asp Leu His Ile Ser Asn Thr Met Ile Arg Lys Gln Gln Ser Ser
1           5           10           15
Val Leu Lys Ile Val Leu Cys Gly Leu Asn Phe
          20           25
  
```

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```

Ser Gln Glu Met Glu Pro Lys Ser
1           5
  
```

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

```

Ser Lys Arg Ile Ala Ser Ile Leu Gln Lys Asn Arg Thr Leu Asn Leu
1           5           10           15
Ser Leu Ile Ser Ile Thr Asn Leu Asp Cys Leu Lys Arg Leu Thr Arg
          20           25           30
Gln Leu His Arg Arg Ser Leu Lys Lys
          35           40
  
```

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Ser Asn Phe Tyr
 1

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Leu Glu Asn Lys Leu Asn Tyr
 1 5

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Tyr Arg Asp Gln Arg Ser Ser Ile Asp Glu Ile Lys Ala Glu Leu Lys
 1 5 10 15
 Leu Asp Asn Lys Lys Tyr Lys Pro Trp Ser Lys Tyr Cys Gly Arg Lys
 20 25 30
 Arg Arg Pro Val Ser Lys Arg Lys Asn Lys Ala Ile Asn Lys Met Ser
 35 40 45
 Thr Glu Val Lys Lys
 50

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Lys Ile Tyr Phe Phe Gln
1 5

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Phe Ile Glu Lys Arg Gly Phe Gly Val Leu Gly Phe Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1007 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser Ala
1 5 10 15

Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser Trp
20 25 30

Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr Lys
35 40 45

Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala Thr
50 55 60

Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys Glu
65 70 75 80

Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu Val
85 90 95

Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln Cys
 100 105 110
 Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu Leu
 115 120 125
 Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp Asn
 130 135 140
 Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr Thr
 145 150 155 160
 Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln Phe
 165 170 175
 Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe Asp
 180 185 190
 Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys
 195 200 205
 Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn
 210 215 220
 Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg Ile
 225 230 235 240
 Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys His
 245 250 255
 Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala Gln
 260 265 270
 Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys Leu
 275 280 285
 Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val Lys
 290 295 300
 Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro Glu
 305 310 315 320
 Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys Thr
 325 330 335
 Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr Thr
 340 345 350
 Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn Ile
 355 360 365
 Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln Lys
 370 375 380
 Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys
 385 390 395 400
 Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln
 405 410 415

Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile
 420 425 430
 Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val
 435 440 445
 Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr
 450 455 460
 Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys
 465 470 475 480
 Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu
 485 490 495
 Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys
 500 505 510
 Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe
 515 520 525
 Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr
 530 535 540
 Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn
 545 550 555 560
 Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp
 565 570 575
 Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly
 580 585 590
 Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp
 595 600 605
 Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu
 610 615 620
 Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys
 625 630 635 640
 Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys
 645 650 655
 Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln
 660 665 670
 Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn
 675 680 685
 Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys
 690 695 700
 Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr
 705 710 715 720
 Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln
 725 730 735

Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu
 740 745 750
 Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu
 755 760 765
 Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu
 770 775 780
 Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile
 785 790 795 800
 Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln
 805 810 815
 Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp
 820 825 830
 Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly
 835 840 845
 Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu
 850 855 860
 Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys
 865 870 875 880
 Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn
 885 890 895
 Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala
 900 905 910
 Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met
 915 920 925
 Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met
 930 935 940
 Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr
 945 950 955 960
 Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe
 965 970 975
 Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe
 980 985 990
 Ile Glu Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys
 995 1000 1005

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Glu	Leu	Glu	Leu	Glu	Met	Gln	Glu	Asn	Gln	Asn	Asp	Ile	Gln	Val	Arg	1	5	10	15
Val	Lys	Ile	Asp	Asp	Pro	Lys	Gln	Tyr	Leu	Val	Asn	Val	Thr	Ala	Ala	20	25	30	
Cys	Leu	Leu	Gln	Glu	Gly	Ser	Tyr	Tyr	Gln	Asp	Lys	Asp	Glu	Arg	Arg	35	40	45	
Tyr	Ile	Ile	Thr	Lys	Ala	Leu	Leu	Glu	Val	Ala	Glu	Ser	Asp	Pro	Glu	50	55	60	
Phe	Ile	Cys	Gln	Leu	Ala	Val	Tyr	Ile	Arg	Asn	Glu	Leu	Tyr	Ile	Arg	65	70	75	80
Thr	Thr	Thr	Asn	Tyr	Ile	Val	Ala	Phe	Cys	Val	Val	His	Lys	Asn	Thr	85	90	95	
Gln	Pro	Phe	Ile	Glu	Lys	Tyr	Phe	Asn	Lys	Ala	Val	Leu	Leu	Pro	Asn	100	105	110	
Asp	Leu	Leu	Glu	Val	Cys	Glu	Phe	Ala	Gln	Val	Leu	Tyr	Ile	Phe	Asp	115	120	125	
Ala	Thr	Glu	Phe	Lys	Asn	Leu	Tyr	Leu	Asp	Arg	Ile	Leu	Ser	Gln	Asp	130	135	140	
Ile	Arg	Lys	Glu	Leu	Thr	Phe	Arg	Lys	Cys	Leu	Gln	Arg	Cys	Val	Arg	145	150	155	160
Ser	Lys	Phe	Ser	Glu	Phe	Asn	Glu	Tyr	Gln	Leu	Gly	Lys	Tyr	Cys	Thr	165	170	175	
Glu	Ser	Gln	Arg	Lys	Lys	Thr	Met	Phe	Arg	Tyr	Leu	Ser	Val	Thr	Asn	180	185	190	
Lys	Gln	Lys	Trp	Asp	Gln	Thr	Lys	Lys	Lys	Arg	Lys	Glu	Asn	Leu	Leu	195	200	205	
Thr	Lys	Leu	Gln	Ala	Ile	Lys	Glu	Ser	Glu	Asp	Lys	Ser	Lys	Arg	Glu	210	215	220	
Thr	Gly	Asp	Ile	Met	Asn	Val	Glu	Asp	Ala	Ile	Lys	Ala	Leu	Lys	Pro	225	230	235	240
Ala	Val	Met	Lys	Lys	Ile	Ala	Lys	Arg	Gln	Asn	Ala	Met	Lys	Lys	His	245	250	255	
Met	Lys	Ala	Pro	Lys	Ile	Pro	Asn	Ser	Thr	Leu	Glu	Ser	Lys	Tyr	Leu	260	265	270	
Thr	Phe	Lys	Asp	Leu	Ile	Lys	Phe	Cys	His	Ile	Ser	Glu	Pro	Lys	Glu	275	280	285	
Arg	Val	Tyr	Lys	Ile	Leu	Gly	Lys	Lys	Tyr	Pro	Lys	Thr	Glu	Glu	Glu	290	295	300	

Tyr Lys Ala Ala Phe Gly Asp Ser Ala Ser Ala Pro Phe Asn Pro Glu
 305 310 315 320
 Leu Ala Gly Lys Arg Met Lys Ile Glu Ile Ser Lys Thr Trp Glu Asn
 325 330 335
 Glu Leu Ser Ala Lys Gly Asn Thr Ala Glu Val Trp Asp Asn Leu Ile
 340 345 350
 Ser Ser Asn Gln Leu Pro Tyr Met Ala Met Leu Arg Asn Leu Ser Asn
 355 360 365
 Ile Leu Lys Ala Gly Val Ser Asp Thr Thr His Ser Ile Val Ile Asn
 370 375 380
 Lys Ile Cys Glu Pro Lys Ala Val Glu Asn Ser Lys Met Phe Pro Leu
 385 390 395 400
 Gln Phe Phe Ser Ala Ile Glu Ala Val Asn Glu Ala Val Thr Lys Gly
 405 410 415
 Phe Lys Ala Lys Lys Arg Glu Asn Met Asn Leu Lys Gly Gln Ile Glu
 420 425 430
 Ala Val Lys Glu Val Val Glu Lys Thr Asp Glu Glu Lys Lys Asp Met
 435 440 445
 Glu Leu Glu Gln Thr Glu Glu Gly Glu Phe Val Lys Val Asn Glu Gly
 450 455 460
 Ile Gly Lys Gln Tyr Ile Asn Ser Ile Glu Leu Ala Ile Lys Ile Ala
 465 470 475 480
 Val Asn Lys Asn Leu Asp Glu Ile Lys Gly His Thr Ala Ile Phe Ser
 485 490 495
 Asp Val Ser Gly Ser Met Ser Thr Ser Met Ser Gly Gly Ala Lys Lys
 500 505 510
 Tyr Gly Ser Val Arg Thr Cys Leu Glu Cys Ala Leu Val Leu Gly Leu
 515 520 525
 Met Val Lys Gln Arg Cys Glu Lys Ser Ser Phe Tyr Ile Phe Ser Ser
 530 535 540
 Pro Ser Ser Gln Cys Asn Lys Cys Tyr Leu Glu Val Asp Leu Pro Gly
 545 550 555 560
 Asp Glu Leu Arg Pro Ser Met Gln Lys Leu Leu Gln Glu Lys Gly Lys
 565 570 575
 Leu Gly Gly Gly Thr Asp Phe Pro Tyr Glu Cys Ile Asp Glu Trp Thr
 580 585 590
 Lys Asn Lys Thr His Val Asp Asn Ile Val Ile Leu Ser Asp Met Met
 595 600 605
 Ile Ala Glu Gly Tyr Ser Asp Ile Asn Val Arg Gly Ser Ser Ile Val
 610 615 620

Asn Ser Ile Lys Lys Tyr Lys Asp Glu Val Asn Pro Asn Ile Lys Ile
 625 630 635 640
 Phe Ala Val Asp Leu Glu Gly Tyr Gly Lys Cys Leu Asn Leu Gly Asp
 645 650 655
 Glu Phe Asn Glu Asn Asn Tyr Ile Lys Ile Phe Gly Met Ser Asp Ser
 660 665 670
 Ile Leu Lys Phe Ile Ser Ala Lys Gln Gly Gly Ala Asn Met Val Glu
 675 680 685
 Val Ile Lys Asn Phe Ala Leu Gln Lys Ile Gly
 690 695

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp Asn Gln Val
 1 5 10 15
 Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr Thr Lys Tyr
 20 25 30
 Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln Phe Cys Gly
 35 40 45
 Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe Asp Lys Lys
 50 55 60
 Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys Ser Thr
 65 70 75 80
 Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn Asn Ile
 85 90 95
 Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg Ile Phe Tyr
 100 105 110
 Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys His Glu Phe
 115 120 125
 Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala Gln Thr Ile
 130 135 140
 Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys Leu Lys Asp
 145 150 155 160
 Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val Lys Asp Phe
 165 170 175

Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro Glu Asn Trp
 180 185 190
 Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys Thr Arg Glu
 195 200 205
 Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr Thr Asp Asn
 210 215 220
 Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn Ile Leu Pro
 225 230 235 240
 Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln Lys Lys Val
 245 250 255
 Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys Asn Leu
 260 265 270
 Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln Val Glu
 275 280 285
 Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile Tyr Val
 290 295 300
 Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val Ser Leu
 305 310 315 320
 Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys
 325 330 335
 Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys Met Ser
 340 345 350
 Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu Lys Glu
 355 360 365
 Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg
 370 375 380
 Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys
 385 390 395 400
 Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr
 405 410 415
 Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met
 420 425 430
 Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met
 435 440 445
 Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro
 450 455 460
 Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val
 465 470 475 480
 Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser
 485 490 495

Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys Asn Asn
 500 505 510
 Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys Asp Tyr
 515 520 525
 Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln Tyr Pro
 530 535 540
 Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn Ala Lys
 545 550 555 560
 Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys Lys Asp
 565 570 575
 Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr Ile Asn
 580 585 590
 Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu
 595 600 605
 Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu
 610 615 620
 Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn Pro
 625 630 635 640
 Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr
 645 650 655
 Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val
 660 665 670
 Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser
 675 680 685
 Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp Ser Val
 690 695 700
 Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly Ile Ser
 705 710 715 720
 Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu Arg Ile
 725 730 735
 Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys Lys Ala
 740 745 750
 Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn Asn Ile
 755 760 765
 Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala Asn Lys
 770 775 780
 Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met Gln Cys
 785 790 795 800
 Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met Ser Ser
 805 810 815

Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr Arg Ala
 820 825 830

Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe Gly Glu
 835 840 845

Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe Ile Glu
 850 855 860

Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys Met Ile Leu
 865 870 875 880

Lys Ala Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln Ser Leu Ile
 885 890 895

Gln

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Met Ser Arg Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu
 1 5 10 15

Thr Asn Leu Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln
 20 25 30

Ile Glu His Tyr Lys Thr Gln Gln Gln Gln Ile Lys Glu Glu Asp Leu
 35 40 45

Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn
 50 55 60

Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu
 65 70 75 80

Arg Arg Val Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val
 85 90 95

Gly Ser Lys Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys
 100 105 110

Lys Asn Gly Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr
 115 120 125

Ile Thr Glu Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp
 130 135 140

Tyr Gln Leu Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg
 145 150 155 160

Glu Thr Asp Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln
 165 170 175
 Lys Asn Tyr Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp
 180 185 190
 Trp Leu Lys Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val
 195 200 205
 Ser Ile Asn Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp
 210 215 220
 Phe Ser Gln Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn
 225 230 235 240
 Ile Asp Val Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg
 245 250 255
 Phe Leu Leu Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser
 260 265 270
 Tyr Thr Arg Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu
 275 280 285
 Thr Ile Phe Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His
 290 295 300
 Leu Gln Val Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser
 305 310 315 320
 Gln Ile Ser Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr
 325 330 335
 Asp Leu Lys Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe
 340 345 350
 Leu Gln Glu Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro
 355 360 365
 Val Ser Ala Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys
 370 375 380
 Val Lys His Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn
 385 390 395 400
 Phe Asp Phe Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly
 405 410 415
 Leu Glu Pro Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Leu
 420 425 430
 Ser Ile Lys Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr
 435 440 445
 Thr Tyr Val Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala
 450 455 460
 Thr Thr Ile Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro
 465 470 475 480

Glu Thr Lys Asp	Glu Thr Pro Ser	Glu Ser Thr Ser	Gly Met Lys Phe
485		490	495
Phe Asp His Leu	Ser Glu Leu Thr	Glu Leu Glu Asp	Phe Ser Val Asn
500		505	510
Leu Gln Ala Thr	Gln Glu Ile Tyr	Asp Ser Leu His	Lys Leu Leu Ile
515		520	525
Arg Ser Thr Asn	Leu Lys Lys Phe	Lys Leu Ser Tyr	Lys Tyr Glu Met
530		535	540
Glu Lys Ser Lys	Met Asp Thr Phe	Ile Asp Leu Lys	Asn Ile Tyr Glu
545		550	555
Thr Leu Asn Asn	Leu Lys Arg Cys	Ser Val Asn Ile	Ser Asn Pro His
	565	570	575
Gly Asn Ile Ser	Tyr Glu Leu Thr	Asn Lys Asp Ser	Thr Phe Tyr Lys
	580	585	590
Phe Lys Leu Thr	Leu Asn Gln Glu	Leu Gln His Ala	Lys Tyr Thr Phe
	595	600	605
Lys Gln Asn Glu	Phe Gln Phe Asn	Asn Val Lys Ser	Ala Lys Ile Glu
	610	615	620
Ser Ser Ser Leu	Glu Ser Leu Glu	Asp Ile Asp Ser	Leu Cys Lys Ser
	625	630	635
Ile Ala Ser Cys	Lys Asn Leu Gln	Asn Val Asn Ile	Ile Ala Ser Leu
	645	650	655
Leu Tyr Pro Asn	Asn Ile Gln Lys	Asn Pro Phe Asn	Lys Pro Asn Leu
	660	665	670
Leu Phe Phe Lys	Gln Phe Glu Gln	Leu Lys Asn Leu	Glu Asn Val Ser
	675	680	685
Ile Asn Cys Ile	Leu Asp Gln His	Ile Leu Asn Ser	Ile Ser Glu Phe
	690	695	700
Leu Glu Lys Asn	Lys Lys Ile Lys	Ala Phe Ile Leu	Lys Arg Tyr Tyr
	705	710	715
Leu Leu Gln Tyr	Tyr Leu Asp Tyr	Thr Lys Leu Phe	Lys Thr Leu Gln
	725	730	735
Gln Leu Pro Glu	Leu Asn Gln Val	Tyr Ile Asn Gln	Gln Leu Glu Glu
	740	745	750
Leu Thr Val Ser	Glu Val His Lys	Gln Val Trp Glu	Asn His Lys Gln
	755	760	765
Lys Ala Phe Tyr	Glu Pro Leu Cys	Glu Phe Ile Lys	Glu Ser Ser Gln
	770	775	780
Thr Leu Gln Leu	Ile Asp Phe Asp	Gln Asn Thr Val	Ser Asp Asp Ser
	785	790	795
			800

Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr
 805 810 815

Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn
 820 825 830

Glu Glu Ile Gln Glu Leu Leu Lys
 835 840

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
 1 5 10 15

Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
 20 25 30

Leu Leu

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser
 1 5 10 15

Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu
 20 25 30

Gly Phe Leu
 35

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Leu	Met	Arg	Leu	Thr	Asp	Asp	Tyr	Leu	Leu	Ile	Thr	Thr	Gln	Glu	Asn
1				5				10					15		
Asn	Ala	Val	Leu	Phe	Ile	Glu	Lys	Leu	Ile	Asn	Val	Ser	Arg	Glu	Asn
		20					25					30			
Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu	Gln	Thr					
		35				40									

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Gln	Asp	Tyr	Cys	Asp	Trp	Ile	Gly	Ile	Ser	Ile
1			5				10			

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Lys	Asn	Arg	Asn	Leu	His	Cys	Thr	Tyr	Ile	Asp	Tyr	Lys	Lys	Ala	Phe
1			5					10					15		
Asp	Ser	Ile	Pro	His	Ser	Trp	Leu	Ile	Gln	Val	Leu	Glu	Ile	Tyr	Lys
		20					25				30				
Ile	Asn														

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Arg	Gln	Ile	Ala	Ile	Lys	Lys	Gly	Ile	Tyr	Gln	Gly	Asp	Ser	Leu	Ser
1				5					10					15	
Pro	Leu	Trp	Phe	Cys	Leu	Ala	Leu	Asn	Pro	Leu	Ser	His	Gln	Leu	His
			20					25					30		
Asn	Asp	Arg													
		35													

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

His	Leu	Ile	Tyr	Met	Asp	Asp	Ile	Lys	Leu	Tyr	Ala	Lys	Asn	Asp	Lys
1				5					10					15	
Glu	Met	Lys	Lys	Leu	Ile	Asp	Thr	Thr	Thr	Ile	Phe	Ser	Asn	Asp	Ile
			20					25					30		
Ser	Met	Gln	Phe	Gly	Leu	Asp	Lys	Cys	Lys	Thr					
		35					40								

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Lys	Cys	Leu	Tyr	Lys	Tyr	Leu	Gly	Phe	Gln	Gln
1				5					10	

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Phe Gly Gly Ser Asn Trp Phe Arg Glu Val Asp Leu Lys Lys Cys Phe
1 5 10 15

Asp Thr Ile Ser His Asp Leu Ile Ile Lys Glu Leu Lys Arg Tyr Ile
 20 25 30

Ser Asp

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

His Val Pro Val Gly Pro Arg Val Cys Val Gln Gly Ala Pro Thr Ser
1 5 10 15

Pro Ala Leu Cys Asn Ala Val Leu Leu Arg Leu Asp Arg Arg Leu Ala
 20 25 30

Gly Leu Ala
 35

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

Tyr Val Arg Tyr Ala Asp Asp Ile Leu Ile Gly Val Leu Gly Ser Lys
1 5 10 15

Asn

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Lys Ile Ile Lys Arg Asp Leu Asn Asn Phe Leu Asn Ser Leu Gly Leu
 1 5 10 15
 Thr Ile Asn Glu Glu Lys Thr Leu Ile
 20 25

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

Glu Thr Pro Ala Arg Phe Leu Gly Tyr Asn Ile
 1 5 10

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr
 1 5 10 15
 Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr
 20 25 30
 Ile Pro

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser
 1 5 10 15
 Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg
 20 25 30
 Lys Gln Asn
 35

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser His Leu Glu Ile
 1 5 10 15
 Gly

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly
 1 5 10 15
 Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp
 20 25 30
 Met Gly Tyr Glu Leu
 35

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Val Leu Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr
 1 5 10 15
 Asp Ser Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys Asp Ala Leu
 20 25 30
 Lys Asn

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Lys Cys Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser
 1 5 10 15
 Ala Pro Ile Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser
 20 25 30
 Glu Phe Lys
 35

(2) INFORMATION FOR SEQ ID NO:246:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

Ile Arg Ser Lys Ser Ser Lys Gly Ile Phe Arg
1 5 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

```

FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "OTHER"
                        /note= "Xaa = hydrophobic amino acid,
                        selected from Ala, Leu, Ile, Val, Pro,
                        Phe, Trp or Met"

```

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

FAILURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 6

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Xaa Xaa Xaa Xaa Xaa Xaa Gln Gly Xaa Xaa Xaa Ser Pro
 1 5 10

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8..10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Xaa	Xaa	Xaa	Tyr	Xaa	Asp	Asp	Xaa	Xaa	Xaa
1				5					10

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Gly Xaa Xaa Xaa Xaa Xaa Xaa Lys
 1 5

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 6
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 8
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Xaa Xaa Xaa Leu Gly Xaa Xaa Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Tyr Tyr Tyr Arg Lys
1 5

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Gly Lys Leu Arg Ile Ile Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Phe Arg Pro Ile Met Thr Phe
1 5

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe
1 5 10 15

Tyr Arg Lys Ser Val Trp Ser Lys
20

(2) INFORMATION FOR SEQ ID NO:257:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Arg Gln His Leu Lys Arg Val Gln Leu Arg Asp Val Ser Glu Ala Glu
 1 5 10 15
 Val Arg Gln His Arg Glu Ala
 20

(2) INFORMATION FOR SEQ ID NO:258:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
 1 5 10 15
 Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu
 20 25

(2) INFORMATION FOR SEQ ID NO:259:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
 1 5 10 15

Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln
 20 25

(2) INFORMATION FOR SEQ ID NO:260:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
 1 5 10 15
 Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Asp Val Ser
 20 25 30

(2) INFORMATION FOR SEQ ID NO:261:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly
 1 5 10 15
 Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 20 25

(2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

YARACHAARG GHATYCCHYA RGG

(2) INFORMATION FOR SEQ ID NO:263:

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

NGTNATDARD ARRTARTCRT C

(2) INFORMATION FOR SEQ ID NO:264:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Gln Thr Lys Gly Ile Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:265:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

Asp Asp Tyr Leu Leu Ile Thr
1 5

(2) INFORMATION FOR SEQ ID NO:266:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe
 1 5 10 15
 Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu
 20 25 30
 Ser Met Asn Pro Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr
 35 40 45
 Asp Asp Tyr Leu Leu Ile Thr
 50 55

(2) INFORMATION FOR SEQ ID NO:267:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile
 1 5 10 15
 Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg
 20 25 30
 Val Val

(2) INFORMATION FOR SEQ ID NO:268:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile Val Asp Leu
 1 5 10 15
 Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys Ala Ser Pro
 20 25 30
 Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile
 35 40 45
 Ser

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Gln Lys Val Gly Ile Pro Gln Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

CAAAAAGTTG GTATCCCTCA GGG

23

(2) INFORMATION FOR SEQ ID NO:271:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

AGACCAAAGG AATTCCATCA GGCTCAATTC TGTCACTTT TTTGTGTCAT TTCTATATGG 60
 AAGATTTGAT TGATGAATAC CTATCGTTTA CGAAAAAGAA AGGATCAGTG TTGTTACGAG 120
 TAGTCGACGA CTACCTCCTC ATCACC 146

(2) INFORMATION FOR SEQ ID NO:272:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Lys	Gly	Ile	Pro	Ser	Gly	Ser	Ile	Leu	Ser	Ser	Phe	Leu	Cys	His	Phe
1				5				10					15		
Tyr	Met	Glu	Asp	Leu	Ile	Asp	Glu	Tyr	Leu	Ser	Phe	Thr	Lys	Lys	Lys
		20					25					30			
Gly	Ser	Val	Leu	Leu	Arg	Val	Val	Asp	Asp	Tyr	Leu	Leu	Ile	Thr	
	35					40					45				

(2) INFORMATION FOR SEQ ID NO:273:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

GACGATTTC TCTTTATAAC A

21

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Asp	Asp	Phe	Leu	Phe	Ile	Thr
1			5			

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg Leu Ile Thr
1 5 10 15
Asn Leu Arg Lys Arg Phe
20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile
1 5 10 15

Lys Gln Asp Leu Met Phe Arg Ile Val Lys
20 25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```

Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser Ser Phe
1           5           10           15
Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu Ser Phe
          20          25          30

```

(2) INFORMATION FOR SEQ ID NO:279:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

```

Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys
1           5           10           15
Lys Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys
          20          25          30
His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn
          35          40          45
Ser

```

(2) INFORMATION FOR SEQ ID NO:280:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

```

Trp Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr
1           5           10           15
Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp
          20          25          30
Thr Trp

```

(2) INFORMATION FOR SEQ ID NO:281:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Ser	Lys	Met	Arg	Ile	Ile	Pro	Lys	Lys	Ser	Asn	Asn	Glu	Phe	Arg	Ile
1				5					10					15	
Ile	Ala	Ile	Pro	Cys	Arg	Gly	Ala	Asp							
			20					25							

(2) INFORMATION FOR SEQ ID NO:282:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Glu	Leu	Tyr	Phe	Met	Lys	Phe	Asp	Val	Lys	Ser	Cys	Tyr	Asp	Ser	Ile
1				5					10					15	
Pro	Arg	Met	Glu	Cys	Met	Arg	Ile	Leu	Lys						
			20					25							

(2) INFORMATION FOR SEQ ID NO:283:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Tyr	Ile	Arg	Glu	Asp	Gly	Leu	Phe	Gln	Gly	Ser	Ser	Leu	Ser	Ala	Pro
1				5					10					15	
Ile	Val	Asp	Leu	Val	Tyr	Asp	Asp	Leu	Leu	Glu	Phe	Tyr	Ser	Glu	Phe
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:284:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

```

Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln
1           5           10           15
Gln Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys
          20           25           30
Tyr Asn Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala Val Ser Ser Gln
          35           40           45
Ser

```

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
1           5           10           15
Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
          20           25           30
Asn Ile Trp
          35

```

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```

Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met
1           5           10           15
Thr Phe Asn Lys Lys Ile Val
          20

```

(2) INFORMATION FOR SEQ ID NO:287:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val
1 5 10 15

Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys
20 25

(2) INFORMATION FOR SEQ ID NO:288:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile
1 5 10 15

Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu Gly Phe
20 25 30

(2) INFORMATION FOR SEQ ID NO:289:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu
1 5 10 15

Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu
20 25 30

Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser Phe Pro Leu
 35 40 45

Ser

(2) INFORMATION FOR SEQ ID NO:290:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Xaa Pro Gln Gly
 1

(2) INFORMATION FOR SEQ ID NO:291:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: 5

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Asp Asp Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln
1 5 10 15

Lys Ser Tyr Ser Lys Thr
20

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro Lys Lys
1 5 10 15

Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val
20 25 30

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser
1 5 10 15

Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys
20 25

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys
1 5 10 15

Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala
20 25

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile
1 5 10 15

Thr Thr Gln Glu Asn Asn
20

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Asn	Val	Ser	Arg	Glu	Asn	Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Phe	Ile	Ile	Pro	Ile	Leu	Gln	Ser	Phe	Phe	Tyr	Ile	Thr	Glu	Ser	Ser
1			5					10					15		
Asp Leu Arg Asn Arg Thr															
20															

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Gln	Lys	Thr	Thr	Leu	Pro	Pro	Ala	Val	Ile	Arg	Leu	Leu	Pro	Lys	Lys
1				5					10				15		
Asn Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu															
20 25 30															

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg
 1 5 10 15

Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys
 20 25

(2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile
 1 5 10 15

Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu
 20 25

(2) INFORMATION FOR SEQ ID NO:302:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile
 1 5 10 15

Thr Val Asn Lys Lys Asp
 20

(2) INFORMATION FOR SEQ ID NO:303:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His Asn Phe Ser Thr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr Glu Ile Ser
 1 5 10 15
 Ser Thr Val Thr Ile Val
 20

(2) INFORMATION FOR SEQ ID NO:305:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Thr Leu Ser Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys
 1 5 10 15
 Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp
 20 25 30

(2) INFORMATION FOR SEQ ID NO:306:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser
 1 5 10 15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Glu Asp Lys Cys Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser
 1 5 10 15
 Leu Ser Ala Pro Ile Val Asp Leu Val Tyr Asp
 20 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile
1 5 10 15

Ser Thr Asp Gln Gln Gln
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:313:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

Arg	Ala	Thr	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile
1				5					10					15	
Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly					
			20					25							

(2) INFORMATION FOR SEQ ID NO:314:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val
1				5					10					15	
Thr	Pro	His	Leu	Thr	His										
			20												

(2) INFORMATION FOR SEQ ID NO:315:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	Val
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:316:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

Ala	Ala	Leu	Arg	Pro	Ala	Ala	His	Val	Gly	Ser	Pro	Gly	Pro	Gly	His	1	5	10	15
Pro	Arg	Asp	Ala	Ala	Arg	Ser	Pro	Leu	Pro	Ser	Arg	Ala	Leu	Pro	Ala	20	25	30	
Ala	Gln	Pro	Leu	Pro	Arg	Gly	Ala	Ala	Ala	Gly	His	Val	Arg	Ala	Ala	35	40	45	
Pro	Gly	Ala	Pro	Gly	Leu	Ala	Gly	Ala	Ala	Arg	Gly	Pro	Gly	Gly		50	55	60	
Phe	Pro	Arg	Xaa	Gly	Gly	Pro	Xaa	Xaa	Gly	Val	Arg	Ala	Leu	Gly	Xaa	65	70	75	80
Xaa	Ala	Ala	Pro	Arg	Arg	Pro	Leu	Leu	Pro	Pro	Gly	Val	Leu	Pro	Glu	85	90	95	
Xaa	Xaa	Gly	Gly	Pro	Ser	Ala	Ala	Xaa	Ala	Val	Arg	Xaa	Arg	Arg	Glu	100	105	110	
Xaa	Arg	Ala	Gly	Leu	Arg	Leu	Arg	Ala	Ala	Gly	Arg	Gly	Pro	Arg	Gly	115	120	125	
Pro	Pro	Arg	Gly	Leu	His	His	Gln	Arg	Ala	Gln	Leu	Pro	Ala	Gln	His	130	135	140	
Gly	Asp	Arg	Arg	Thr	Ala	Gly	Glu	Arg	Gly	Val	Gly	Ala	Ala	Ala	Ala	145	150	155	160
Pro	Arg	Gly	Arg	Arg	Arg	Ala	Gly	Ser	Pro	Ala	Gly	Thr	Leu	Arg	Xaa	165	170	175	
Xaa	Cys	Ala	Gly	Gly	Ser	Gln	Leu	Arg	Leu	Pro	Xaa	Val	Arg	Ala	Ala	180	185	190	
Ala	Val	Pro	Ala	Arg	Arg	Cys	Xaa	Ser	Gly	Pro	Ala	Pro	Ala	Thr	Arg	195	200	205	
Xaa	Trp	Thr	Arg	Xaa	Arg	Leu	Gly	Ser	Asn	Gly	Pro	Gly	Thr	Ile	Ala	210	215	220	
Ser	Gly	Arg	Pro	Gly	Ser	Pro	Trp	Ala	Ala	Ser	Pro	Gly	Cys	Glu	Glu	225	230	235	240
Ala	Arg	Gly	Gln	Cys	Gln	Pro	Lys	Ser	Ala	Val	Ala	Gln	Glu	Ala	Gln	245	250	255	
Ala	Trp	Arg	Cys	Pro												260			

(2) INFORMATION FOR SEQ ID NO:317:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Ala	Gly	Ala	Asp	Ala	Arg	Trp	Ala	Gly	Val	Leu	Gly	Pro	Pro	Gly	Gln
1				5					10					15	
Asp Ala Trp Thr Glu															
20															

(2) INFORMATION FOR SEQ ID NO:318:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Pro	Trp	Phe	Leu	Cys	Gly	Val	Thr	Cys	Gln	Thr	Arg	Arg	Arg	Ser	His
1				5					10					15	
Leu	Phe	Gly	Gly	Cys	Ala	Leu	Trp	His	Ala	Pro	Leu	Pro	Pro	Ile	Arg
			20					25						30	
Gly	Pro	Pro	Ala	Pro	Arg	Gly	Pro	Pro	Ile	His	Ile	Ala	Ala	Thr	Thr
			35				40					45			
Ser	Trp	Asp	Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe
		50				55					60				
Leu	Tyr	Ser	Ser	Gly	Asp	Lys	Xaa	Thr	Ala	Xaa	Leu	Leu	Pro	Thr	Gln
65					70					75					80
Tyr Ile															

(2) INFORMATION FOR SEQ ID NO:319:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

[illegible]

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

[illegible]

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

Val	Cys	Thr	Ser	Ser	Ser	Cys	Ser	Gly	Leu	Ser	Phe	Met	Ser	Arg	Arg
1				5				10						15	
Pro	Arg	Phe	Lys	Arg	Thr	Gly	Ser	Phe	Ser	Thr	Gly	Arg	Val	Ser	Gly
			20					25					30		
Ala	Ser	Cys	Lys	Ala	Leu	Glu	Ser	Asp	Ser	Thr					
		35					40								

(2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Arg	Gly	Cys	Ser	Cys	Gly	Ser	Cys	Arg	Lys	Gln	Arg	Ser	Gly	Ser	Ile
1				5				10						15	
Gly	Lys	Pro	Gly	Pro	Pro	Cys									
			20												

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Arg	Pro	Asp	Ser	Ala	Ser	Ser	Pro	Ser	Leu	Thr	Gly	Cys	Gly	Arg	Leu
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

```

Thr Trp Thr Thr Ser Trp Glu Pro Glu Arg Ser Ala Glu Lys Arg Gly
1           5           10           15

Pro Ser Val Ser Pro Arg Gly
          20

```

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

```

Arg His Cys Ser Ala Cys Ser Thr Thr Ser Gly Arg Gly Ala Pro Ala
1           5           10           15

Ser Trp Ala Pro Leu Cys Trp Ala Trp Thr Ile Ser Thr Gly Pro Gly
          20           25           30

Ala Pro Ser Cys Cys Val Cys Gly Pro Arg Thr Arg Arg Leu Ser Cys
          35           40           45

Thr Leu Ser Arg Trp Met
          50

```

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```

Arg Ala Arg Thr Thr Pro Ser Pro Arg Thr Gly Ser Arg Arg Ser Ser
1           5           10           15

Pro Ala Ser Ser Asn Pro Arg Thr Arg Thr Ala Cys Val Gly Met Pro
          20           25           30

Trp Ser Arg Arg Pro Pro Met Gly Thr Ser Ala Arg Pro Ser Arg Ala
          35           40           45

```

Thr Ser Leu Pro
50

(2) INFORMATION FOR SEQ ID NO:327:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

Gln Thr Ser Ser Arg Thr Cys Asp Ser Ser Trp Leu Thr Cys Arg Xaa
 1 5 10 15

Thr Ala Arg

(2) INFORMATION FOR SEQ ID NO:328:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Gly Met Pro Ser Ser Ser Ser Arg Ala Pro Pro
 1 5 10

(2) INFORMATION FOR SEQ ID NO:329:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

Met Arg Pro Ala Val Ala Ser Ser Thr Ser Ser Tyr Ala Ser Cys Ala
 1 5 10 15

Thr Thr Pro Cys Ala Ser Gly Ala Ser Pro Thr Ser Ser Ala Arg Gly
 20 25 30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

His Leu Thr Ser Pro Thr Arg Lys Pro Ser Ser Gly Pro Trp Ser Glu
1 5 10 15
Val Ser Leu Ser Met Ala Ala Trp
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Thr Cys Gly Arg Gln Trp
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Lys Thr Arg Pro Trp Val Ala Arg Leu Leu Phe Arg Cys Arg Pro Thr
 1 5 10 15
 Ala Tyr Ser Pro Gly Ala Ala Cys Cys Trp Ile Pro Gly Pro Trp Arg
 20 25 30
 Cys Arg Ala Thr Thr Pro Ala Met Pro Gly Pro Pro Ser Glu Pro Val
 35 40 45
 Ser Pro Ser Thr Ala Ala Ser Arg Leu Gly Gly Thr Cys Val Ala Asn
 50 55 60
 Ser Leu Gly Ser Cys Gly
 65 70

(2) INFORMATION FOR SEQ ID NO:333:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Ser Val Thr Ala Cys Phe Trp Ile Cys Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:334:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Thr Ala Ser Arg Arg Cys Ala Pro Thr Ser Thr Arg Ser Ser Cys Cys
 1 5 10 15
 Arg Arg Thr Gly Phe Thr His Val Cys Cys Ser Ser His Phe Ile Ser
 20 25 30
 Lys Phe Gly Arg Thr Pro His Phe Ser Cys Ala Ser Ser Leu Thr Arg
 35 40 45
 Pro Pro Ser Ala Thr Pro Ser
 50 55

(2) INFORMATION FOR SEQ ID NO:335:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

Leu Cys Pro Pro Arg Pro Cys Ser Gly Cys Ala Thr Lys His Ser Cys
20 25 30

Ser Ser

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

Leu Asp Thr Val Ser Pro Thr Cys His Ser Trp Gly His Ser Gly Gln
1 5 10 15

Pro Arg Arg Ser
20

(2) INFORMATION FOR SEO ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

Val Gly Ser Ser Arg Gly Arg Arg
1 5

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

```

Leu Pro Trp Arg Pro Gln Pro Thr Arg His Cys Pro Gln Thr Ser Arg
1           5           10           15
Pro Ser Trp Thr Asp Gly His Pro Pro Thr Ala Arg Pro Arg Ala Asp
          20           25           30
Thr Ser Ser Pro Val Thr Pro Gly Ser Thr Ser Gln Gly Gly Arg Gly
          35           40           45
Gly Pro His Pro Gly Pro His Arg Trp Glu Ser Glu Ala
          50           55           60

```

(2) INFORMATION FOR SEQ ID NO:339:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

```

Val Ser Val Trp Pro Arg Pro Ala Cys Pro Ala Glu Gly
1           5           10

```

(2) INFORMATION FOR SEQ ID NO:340:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

```

Gly Leu Ser Glu Cys Pro Ala Lys Gly
1           5

```

(2) INFORMATION FOR SEQ ID NO:341:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Val	Ser	Ser	Thr	Pro	Ala	Val	Phe	Thr	Ser	Pro	Gln	Ala	Gly	Ala	Arg
1				5				10					15		
Leu	His	Pro	Arg	Ala	Ser	Phe	Ser	Ser	Pro	Gly	Ala	Arg	Leu	Pro	Leu
			20				25						30		
Pro	Thr														

(2) INFORMATION FOR SEQ ID NO:342:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Ser	Ile	Pro	Arg	Phe	Ala	Ile	Val	His	Pro	Ser	Pro	Cys	Pro	Pro	Leu
1				5				10					15		
Pro	Ser	Thr	Pro	Thr	Ile	Gln	Val	Glu	Thr	Leu	Arg	Arg	Thr	Leu	Gly
			20				25						30		
Ala	Leu	Gly	Ile	Trp	Ser	Asp	Gln	Arg	Cys	Ala	Leu	Tyr	Thr	Gly	Glu
		35				40					45				
Asp	Pro	Ala	Pro	Gly	Trp	Gly	Ser	Leu	Trp	Val	Lys	Leu	Gly	Gly	Gly
	50					55				60					
Ala	Val	Gly	Val	Lys	Tyr										
65					70										

(2) INFORMATION FOR SEQ ID NO:343:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

Ile	Tyr	Glu	Phe	Phe	Ser	Phe	Glu	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys
1				5				10					15		

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

```

Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro Ala Thr
1           5           10           15

Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu
          20           25           30

Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg
          35           40           45

Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala
50           55           60

Phe Arg Ala Xaa Val Ala Xaa Cys Xaa Val Cys Val Pro Trp Xaa Xaa
65           70           75           80

Xaa Xaa Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Xaa
          85           90           95

Xaa Leu Val Ala Arg Val Leu Xaa Xaa Leu Cys Xaa Arg Gly Ala Xaa
100          105          110

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
115          120          125

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
130          135          140

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
145          150          155          160

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Xaa
          165          170          175

Phe Val Leu Val Xaa Pro Ser Cys Ala Tyr Xaa Val Cys Gly Pro Pro
180          185          190

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala
195          200          205

Xaa Gly Pro Glu Xaa Val Trp Asp Pro Thr Gly Leu Glu Pro
210          215          220

```

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

```

Arg Gln Gly Gly Arg Gly Pro Pro Gly Leu Pro Ala Pro Gly Ala Arg
1           5           10           15
Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro
20           25           30
Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly
35           40           45
Ser Trp Ala His Pro Gly Arg Thr Pro Gly Pro Ser Asp Arg Gly Phe
50           55           60
Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu
65           70           75           80
Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln
85           90           95
His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Gly Thr
100          105          110
Arg Leu Val Pro Arg Cys Thr Pro Arg Pro Ser Thr Ser Ser Thr Pro
115          120          125
Gln Ala Thr Xaa Thr Leu Arg Pro Ser Phe Leu Leu Asn Ile Ser Glu
130          135          140
Ala Gln Pro Asp Trp Arg Ser Gly Gly Ser Trp Arg Xaa Ser Phe Trp
145          150          155          160
Phe Gln Ala Leu Asp Ala Arg Ile Pro Arg Arg Leu Pro Arg Leu Pro
165          170          175
Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn
180          185          190
His Ala Gln Cys Pro Tyr Gly Val Phe Leu Lys Thr His Cys Pro Leu
195          200          205
Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro
210          215          220
Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Glu His Arg Pro Pro Ser
225          230          235          240
Pro Gly Ala Ala Ala Pro Pro Ala Gln Gln Pro Leu Ala Gly Val Arg
245          250          255
Leu Arg Ala Gly Leu Pro Ala Pro Ala Gly Ala Pro Arg Pro Leu Gly
260          265          270

```

Leu Gln Ala Gln Arg Thr Pro Leu Pro Gln Glu His Gln Glu Val His
 275 280 285
 Leu Pro Gly Glu Ala Cys Gln Ala Leu Ala Ala Gly Ala Asp Val Glu
 290 295 300
 Asp Glu Arg Ala Gly Leu Arg Leu Ala Ala Gln Glu Pro Arg Gly Trp
 305 310 315 320
 Leu Cys Ser Gly Arg Arg Ala Pro Ser Ala
 325 330

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Gly Asp Pro Gly Gln Val Pro Ala Leu Ala Asp Glu Cys Val Arg Arg
 1 5 10 15
 Arg Ala Ala Gln Val Phe Leu Leu Cys His Gly Asp His Val Ser Lys
 20 25 30
 Glu Gln Ala Leu Phe Leu Pro Glu Glu Cys Leu Glu Gln Val Ala Lys
 35 40 45
 His Trp Asn Gln Thr Ala Leu Glu Glu Gly Ala Ala Ala Gly Ala Val
 50 55 60
 Gly Ser Arg Gly Gln Ala Ala Ser Gly Ser Gln Ala Arg Pro Ala Asp
 65 70 75 80
 Val Gln Thr Pro Leu His Pro Gln Ala
 85

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Arg Ala Ala Ala Asp Cys Glu His Gly Leu Arg Arg Gly Ser Gln Asn
 1 5 10 15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Ala 1	Val	Leu	Cys	Gln 5	Gly	Gly	Cys	Asp	Gly 10	Arg	Val	Arg	His	His 15	Pro
Pro	Gly	Gln	Ala 20	His	Gly	Gly	His	Arg 25	Gln	His	His	Gln	Thr 30	Pro	Glu
His	Val	Leu	Arg	Ala	Ser	Val	Cys 40	Arg	Gly	Pro	Glu	Gly 45	Arg	Pro	Trp
Ala 50	Arg	Pro	Gln	Gly	Leu	Gln 55	Glu	Pro	Arg	Leu	Tyr 60	Leu	Asp	Arg	Pro
Pro 65	Ala	Val	His	Ala	Thr 70	Val	Arg	Gly	Ser	Pro 75	Ala	Gly	Xaa	Gln	Pro 80
Ala	Glu	Gly	Cys	Arg 85	Arg	His	Arg	Ala	Glu 90	Leu	Leu	Pro	Glu		

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Gly Gln Gln Trp Pro Leu Arg Arg Leu Pro Thr Leu His Val Pro Pro
1 5 10 15

Arg Arg Ala His Gln Gly Gln Val Leu Arg Pro Val Pro Gly Asp Pro
 20 25 30

Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg
 35 40 45

His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro
 50 55 60

Ala Phe Gly Gly
 65

(2) INFORMATION FOR SEQ ID NO:350:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Phe Leu Val Gly Asp Thr Ser Pro His Pro Arg Glu Asn Leu Pro Gln
 1 5 10 15

Asp Pro Gly Pro Arg Cys Pro
 20

(2) INFORMATION FOR SEQ ID NO:351:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Val Trp Leu Arg Gly Glu Leu Ala Glu Asp Ser Gly Glu Leu Pro Cys
 1 5 10 15

Arg Arg Arg Gly Pro Gly Trp His Gly Phe Cys Ser Asp Ala Gly Pro
 20 25 30

Arg Pro Ile Pro Leu Val Arg Pro Ala Ala Gly Tyr Pro Asp Pro Gly
 35 40 45

Gly Ala Glu Arg Leu Leu Gln Leu Cys Pro Asp Leu His Gln Ser Gln
 50 55 60

Ser His Leu Gln Pro Arg Leu Gln Gly Trp Glu Glu His Ala Ser Gln
 65 70 75 80

Thr Leu Trp Gly Leu Ala Ala Glu Val Ser Gln Pro Val Ser Gly Phe
 85 90 95

Ala Gly Glu Gln Pro Pro Asp Gly Val His Gln His Leu Gln Asp Pro
 100 105 110

Pro Ala Ala Gly Val Gln Val Ser Arg Met Cys Ala Ala Pro Ile
 115 120 125

Ser Ser Ala Ser Leu Glu Glu Pro His Ile Phe Pro Ala Arg His Leu
 130 135 140

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

His Gly Leu Pro Leu Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp
 1 5 10 15

Val Ala Gly Gly Gln Gly Arg Arg Arg Pro Ser Ala Leu Arg Gly Arg
 20 25 30

Ala Val Ala Val Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser Thr Pro
 35 40 45

Cys His Leu Arg Ala Thr Pro Gly Val Thr Gln Asp Ser Pro Asp Ala
 50 55 60

Ala Glu Ser Glu Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly Gly Arg
 65 70 75 80

Ser Gln Pro Gly Thr Ala Leu Arg Leu Gln Asp His Pro Gly Leu Met
 85 90 95

Ala Thr Arg Pro Gln Pro Gly Arg Glu Gln Thr Pro Ala Ala Leu Ser
 100 105 110

Arg Arg Ala Leu Arg Pro Arg Glu Gly Gly Ala Ala His Thr Gln Ala
 115 120 125

Arg Thr Ala Gly Ser Leu Arg Pro Glu
 130 135

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

Val	Phe	Gly	Arg	Gly	Leu	His	Val	Arg	Leu	Lys	Ala	Glu	Cys	Pro	Ala
1				5					10					15	
Glu Ala															

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Ala	Ser	Val	Gln	Pro	Arg	Ala	Glu	Cys	Pro	Ala	His	Leu	Pro	Ser	Ser
1				5					10					15	
Leu	Pro	His	Arg	Leu	Ala	Leu	Gly	Ser	Thr	Pro	Gly	Pro	Ala	Phe	Pro
			20					25					30		
His	Gln	Glu	Pro	Gly	Phe	His	Ser	Pro	His	Arg	Asn	Ser	Pro	Ser	Pro
		35					40					45			
Asp	Ser	Pro	Leu	Phe	Thr	Pro	Arg	Pro	Ala	Leu	Leu	Cys	Leu	Pro	Pro
	50						55				60				
Pro	Pro	Ser	Arg	Trp	Arg	Pro									
65					70										

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Glu	Gly	Pro	Trp	Glu	Leu	Trp	Glu	Phe	Gly	Val	Thr	Lys	Gly	Val	Pro
1				5					10					15	
Cys	Thr	Gln	Ala	Arg	Thr	Leu	His	Leu	Asp	Gly	Gly	Pro	Cys	Gly	Ser
			20					25					30		

Asn Trp Gly Glu Val Leu Trp Glu
 35 40

(2) INFORMATION FOR SEQ ID NO:356:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

Asn Thr Glu Tyr Met Ser Phe Ser Val Leu Lys Lys Lys Lys Lys Lys
 1 5 10 15

 Lys Lys

(2) INFORMATION FOR SEQ ID NO:357:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

Ser Ala Ala Ser Cys Cys Ala Arg Gly Lys Pro Trp Pro Arg Pro Pro
 1 5 10 15

 Pro Arg Cys Arg Ala Leu Pro Ala Ala Glu Pro Cys Ala Pro Cys Cys
 20 25 30

 Ala Ala Thr Thr Ala Arg Cys Cys Arg Trp Pro Arg Ser Cys Gly Ala
 35 40 45

 Trp Gly Pro Arg Ala Gly Gly Trp Cys Ser Ala Gly Thr Arg Arg Leu
 50 55 60

 Ser Ala Arg Trp Trp Pro Xaa Ala Trp Cys Ala Cys Pro Gly Xaa Xaa
 65 70 75 80

 Gly Xaa Pro Pro Pro Pro Pro Pro Ser Ala Arg Cys Pro Ala
 85 90

(2) INFORMATION FOR SEQ ID NO:358:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

Xaa Xaa Trp Trp Pro Glu Cys Cys Xaa Xaa Cys Ala Xaa Ala Ala Arg
1 5 10 15

Xaa Thr Cys Trp Pro Ser Ala Ser Arg Cys Trp Thr Gly Pro Ala Gly
20 25 30

Ala Pro Pro Arg Pro Ser Pro Pro Ala Cys Ala Ala Thr Cys Pro Thr
35 40 45

Arg

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1003 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

Pro Thr His Cys Gly Gly Ala Gly Arg Gly Gly Cys Cys Cys Ala Ala
1 5 10 15

Trp Ala Thr Thr Cys Trp Phe Thr Cys Trp His Ala Ala Arg Xaa Leu
20 25 30

Cys Trp Trp Xaa Pro Ala Ala Pro Thr Xaa Cys Ala Gly Arg Arg Cys
35 40 45

Thr Ser Ser Ala Leu Xaa Leu Arg Pro Gly Pro Arg His Thr Leu Xaa
50 55 60

Asp Pro Xaa Ala Ser Gly Ile Gln Arg Ala Trp Asn His Ser Val Arg
65 70 75 80

Glu Ala Gly Val Pro Leu Gly Cys Gln Pro Arg Val Arg Gly Gly Ala
85 90 95

Gly Ala Val Pro Ala Glu Val Cys Arg Cys Pro Arg Gly Pro Gly Val
100 105 110

Ala Leu Pro Leu Ser Arg Ser Gly Arg Pro Leu Gly Arg Gly Pro Gly
115 120 125

Pro Thr Arg Ala Gly Arg Leu Asp Arg Val Thr Val Val Ser Val Trp
130 135 140

Cys His Leu Pro Asp Pro Pro Lys Lys Pro Pro Leu Trp Arg Val Arg
145 150 155 160

Ser Leu Ala Arg Ala Thr Pro Thr His Pro Trp Ala Ala Ser Thr Thr
 165 170 175
 Arg Ala Pro His Pro His Arg Gly His His Val Leu Gly His Ala Leu
 180 185 190
 Ser Pro Gly Val Arg Arg Asp Gln Ala Leu Pro Leu Leu Leu Arg Arg
 195 200 205
 Gln Xaa His Cys Xaa Pro Pro Ser Tyr Ser Ile Tyr Leu Arg Pro Ser
 210 215 220
 Leu Thr Gly Val Arg Glu Val Arg Gly Asp Xaa Leu Ser Gly Ser Arg
 225 230 235 240
 Pro Trp Met Pro Gly Phe Pro Ala Gly Cys Pro Ala Cys Pro Ser Xaa
 245 250 255
 Thr Gly Lys Cys Gly Pro Cys Phe Trp Ser Cys Leu Gly Thr Thr Arg
 260 265 270
 Ser Ala Pro Thr Gly Cys Ser Ser Arg Arg Thr Ala Arg Cys Glu Leu
 275 280 285
 Arg Ser Pro Gln Gln Pro Val Ser Val Pro Gly Arg Ser Pro Arg Ala
 290 295 300
 Leu Trp Arg Pro Pro Arg Arg Arg Asn Thr Asp Pro Arg Arg Leu Val
 305 310 315 320
 Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val
 325 330 335
 Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg
 340 345 350
 His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu
 355 360 365
 Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser
 370 375 380
 Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val
 385 390 395 400
 Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu
 405 410 415
 His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe
 420 425 430
 Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg
 435 440 445
 Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu
 450 455 460
 Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His
 465 470 475 480

Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro
 485 490 495
 Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
 500 505 510
 Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
 515 520 525
 Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro
 530 535 540
 Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala
 545 550 555 560
 Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu
 565 570 575
 Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro
 580 585 590
 Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn
 595 600 605
 Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly
 610 615 620
 His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu
 625 630 635 640
 Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Xaa Asn Ser Pro
 645 650 655
 Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala
 660 665 670
 Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala
 675 680 685
 Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
 690 695 700
 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
 705 710 715 720
 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg
 725 730 735
 Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys
 740 745 750
 Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val
 755 760 765
 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala
 770 775 780
 Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro
 785 790 795 800

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

[illegible]

(2) INFORMATION FOR SEQ ID NO:361:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

Gly Leu Ser Glu Cys Leu Ala Glu Ala Cys Met Ser Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO:362:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

Arg Leu Ser Val Arg Leu Arg Pro Glu Arg Val Ser Ser Gln Gly Leu
 1 5 10 15

Ser Val Gln His Thr Cys Arg Leu His Phe Pro Thr Gly Trp Arg Ser
 20 25 30

Ala Pro Pro Gln Gly Gln Leu Phe Leu Thr Arg Ser Pro Ala Ser Thr
 35 40 45

Pro His Ile Gly Ile Val His Pro Gln Ile Arg His Cys Ser Pro Leu
 50 55 60

Ala Leu Pro Ser Phe Ala Phe His Pro His His Pro Gly Gly Asp Pro
 65 70 75 80

Glu Lys Asp Pro Gly Ser Ser Gly Asn Leu Glu
 85 90

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

Pro Lys Val Cys Pro Val His Arg Arg Gly Pro Cys Thr Trp Met Gly
1 5 10 15

Val Pro Val Gly Gln Ile Gly Gly Arg Cys Cys Gly Ser Lys Ile Leu
20 25 30

Asn Ile

(2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Val Phe Gln Phe
1

771
(2) INFORMATION FOR SEQ ID NO:365:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

Lys Lys Lys Lys Lys Lys Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"

/note= "Xaa = polar amino acid,
selected from Gly, Ser, Thr, Tyr, Cys,
Asn or Gln"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

Xaa Phe Phe Tyr
1

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

Xaa Arg Xaa Ile Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,

selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

Phe Arg Xaa Ile
1

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = charged amino acid,
 selected from Asp, Glu, His, Lys or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 6
 (D) OTHER INFORMATION: /product= "OTHER"
 /note= "Xaa = hydrophobic amino acid,
 selected from Ala, Leu, Ile, Val, Pro,
 Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Pro Xaa Leu Tyr Phe Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Gly Ile Pro Gln Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:371:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

Leu Leu Arg Leu
1

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

Asp Asp Phe Leu Xaa Ile Thr
1 5

(2) INFORMATION FOR SEQ ID NO:373:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

Trp	Leu	Tyr	Asn	Ser	Phe	Ile	Ile	Pro	Ile	Leu	Gln	Ser	Phe	Phe	Tyr
1				5				10						15	
Ile	Thr	Glu	Ser	Ser	Asp	Leu	Arg	Asn	Arg	Thr	Val	Tyr	Phe	Arg	Lys
			20					25					30		

Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met Lys Met
 35 40 45

(2) INFORMATION FOR SEQ ID NO:374:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Asn Asn Val Arg Met Asp Thr Gln Lys Thr Thr Leu Pro Pro Ala Val
 1 5 10 15
 Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg Leu Ile Thr Asn Leu
 20 25 30
 Arg Lys Arg Phe Leu Ile Lys Met Gly Ser Asn Lys Lys Met Leu Val
 35 40 45
 Ser Thr Asn Gln Thr Leu
 50

(2) INFORMATION FOR SEQ ID NO:375:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Phe Gly Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr
 1 5 10 15
 Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys Lys Lys Leu
 20 25 30
 Lys Asp

(2) INFORMATION FOR SEQ ID NO:376:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser
 1 5 10 15
 Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu
 20 25 30
 Ser Phe Thr
 35

(2) INFORMATION FOR SEQ ID NO:377:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys Lys
 1 5 10 15
 Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His
 20 25 30
 Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile
 35 40

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	Tyr
1				5					10					15	
Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	Lys
		20						25					30		
Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	Lys
		35					40						45		

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 54 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

Glu	Val	Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg
1				5					10					15	
Leu	Arg	Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met
		20						25					30		
Asp	Tyr	Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu
		35					40					45			
Arg	Leu	Thr	Ser	Arg	Val										
		50													

(2) INFORMATION FOR SEQ ID NO:381:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

Pro	Pro	Pro	Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr
1				5					10					15	
Asp	Thr	Ile	Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile
		20						25					30		

Lys Pro

(2) INFORMATION FOR SEQ ID NO:382:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser
1				5				10						15	
Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe
			20					25					30		
Ala	Gly	Ile													
		35													

(2) INFORMATION FOR SEQ ID NO:383:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr
1				5				10						15	
His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr
			20					25					30		
Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val					
		35					40								

(2) INFORMATION FOR SEQ ID NO:384:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
1 5 10 15

Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
20 25 30

Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp Leu Lys Lys
35 40 45

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys
1 5 10 15

Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe
20 25 30

Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr
35 40 45

Asn Thr Lys Leu Leu Asn
50

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
 1 5 10 15
 Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
 20 25 30
 Leu Leu

(2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser
 1 5 10 15
 Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu
 20 25 30
 Gly Phe Leu
 35

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu Asn
 1 5 10 15
 Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu Asn
 20 25 30
 Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr
 35 40

(2) INFORMATION FOR SEQ ID NO:390:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Gln	Asp	Tyr	Cys	Asp	Trp	Ile	Gly	Ile	Ser	Ile
1				5					10	

(2) INFORMATION FOR SEQ ID NO:391:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

Trp	Leu	Phe	Arg	Gln	Leu	Ile	Pro	Lys	Ile	Ile	Gln	Thr	Phe	Phe	Tyr
1				5					10					15	
Cys	Thr	Glu	Ile	Ser	Ser	Thr	Val	Thr	Ile	Val	Tyr	Phe	Arg	His	Asp
		20						25					30		
Thr	Trp	Asn	Lys	Leu	Ile	Thr	Pro	Phe	Ile	Val	Glu	Tyr	Phe	Lys	
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:392:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

Cys	Arg	Asn	His	Asn	Ser	Tyr	Thr	Leu	Ser	Asn	Phe	Asn	His	Ser	Lys
1				5					10					15	
Met	Arg	Ile	Ile	Pro	Lys	Lys	Ser	Asn	Asn						
		20						25							

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe
 1 5 10 15

Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro
 20 25

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln Gln
 1 5 10 15

Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr
 20 25 30

Asn Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala
 35 40

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

Lys Glu Leu Glu Val Trp Lys His Ser Ser Thr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

```

Leu Ser Asn Glu Leu Gly Thr Gly Lys Phe Lys Phe Lys Pro Met Arg
1              5              10              15

Ile Val Asn Ile Pro Lys Pro Lys Gly Gly Ile Arg Pro Leu Ser Val
              20              25              30

Gly Asn Pro Arg Asp Lys Ile Val Gln Glu Val Met Arg Met Ile Leu
              35              40              45

Asp Thr Ile Phe Asp Lys Lys
50              55

```

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

```

Phe Gly Gly Ser Asn Trp Phe Ile Glu Val Asp Leu Lys Lys Cys Phe
1              5              10              15

Asp Thr Ile Ser His Asp Leu Ile Ile Lys Glu Leu Lys Arg Tyr Ile
              20              25              30

Ser Asp

```

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

```

Thr Tyr His Lys Pro Met Leu Gly Leu Pro Gln Gly Ser Leu Ile Ser
1              5              10              15

```

Pro Ile Leu Cys Asn Ile Val Met Thr Leu Val Asp Asn Trp Leu Glu
 20 25 30

Asp Tyr Ile
 35

(2) INFORMATION FOR SEQ ID NO:399:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

Lys Met Ile Lys Arg Asp Leu Asn Asn Phe Leu Asn Ser Leu Gly Leu
 1 5 10 15

Thr Ile Asn Glu Glu Lys Thr Leu Ile
 20 25

(2) INFORMATION FOR SEQ ID NO:400:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

Arg Cys Val Val Glu Gly Thr Phe Pro Pro Val Trp Lys Asp Gly Arg
 1 5 10 15

Leu Leu Val Leu Pro Lys Gly Asn Gly Arg
 20 25

(2) INFORMATION FOR SEQ ID NO:401:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Tyr Arg Pro Val Thr Leu Leu Pro Val Leu Gly Lys Ile Leu Glu Lys
 1 5 10 15
 Val Leu Leu Gln Cys Ala Pro Gly Leu Thr His Ser Ile
 20 25

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Glu Gln Arg Tyr Val Met Ala Ile Phe Leu Asp Ile Ser Gly Ala Phe
 1 5 10 15
 Asp Asn Ala Trp Trp Pro Met Ile Met Val Lys Ala Lys Arg Asn Cys
 20 25 30
 Pro Pro

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

Glu Trp Lys Val Ser Thr Met Gly Cys Pro Gln Gly Ser Val Leu Gly
 1 5 10 15
 Pro Thr Leu Trp Asn Val Leu Met Asp Asp Leu Leu Ala Leu Pro Gln
 20 25 30
 Gly Ile Glu
 35

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

Met Val Ala Tyr Ala Asp Asp Val Thr Val Leu Val Arg Gly Asp Ser
1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO:405:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

Ala His Ala Val Leu Gly Leu Ala Glu Gly Trp Ala Ser Arg Asn Lys
1 5 10 15

Leu Asp Phe Ala Pro Ala Lys Ser Arg Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:406:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Glu Asn Gln Val Thr Val Leu Gly Val Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:407:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro
 1 5 10 15
 Val Phe Ala Ile Lys Lys Lys Asp Ser Thr
 20 25

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp
 1 5 10 15
 Phe Trp Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys
 20 25 30
 Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val
 35 40 45
 Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro
 50 55 60

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser
 1 5 10 15
 Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Lys
 20 25 30
 Lys Gln Asn
 35

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile
 1 5 10 15
 Gly

(2) INFORMATION FOR SEQ ID NO:411:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly
 1 5 10 15
 Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp
 20 25 30
 Met Gly Ile Thr Leu
 35

(2) INFORMATION FOR SEQ ID NO:412:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 545 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr
 1 5 10 15
 Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser
 20 25 30
 Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu
 35 40 45
 Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro
 50 55 60

Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu
 65 70 75 80
 Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg
 85 90 95
 Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe
 100 105 110
 Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala
 115 120 125
 Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val
 130 135 140
 Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys
 145 150 155 160
 Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr
 165 170 175
 Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg
 180 185 190
 Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala
 195 200 205
 Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg
 210 215 220
 Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val
 225 230 235 240
 Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe
 245 250 255
 Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly
 260 265 270
 Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser
 275 280 285
 Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe
 290 295 300
 Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe
 305 310 315 320
 Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr
 325 330 335
 Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys
 340 345 350
 Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala
 355 360 365
 Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu
 370 375 380

Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala
 385 390 395 400
 Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala
 405 410 415
 Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys
 420 425 430
 His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys
 435 440 445
 Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala
 450 455 460
 Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr
 465 470 475 480
 Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile
 485 490 495
 Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala
 500 505 510
 Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe
 515 520 525
 Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly
 530 535 540
 Ser
 545

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

Ser Gln His Xaa Gln Thr Leu Leu Ala Ala Met Pro Ile Ser Arg Leu
 1 5 10 15
 Arg Phe Ile Pro Lys Pro Asn Trp Arg Pro Ile Val Asn Met Ser Tyr
 20 25 30
 Ser Met Gly Ala Arg Ala Leu Gly Arg Arg Lys Gln Ala Gln His Phe
 35 40 45
 Thr Gln Arg Leu Lys Thr Leu Phe Ser Met Leu Asn Tyr Glu Pro Glu
 50 55 60
 Pro Asp Ile Lys Leu Ile Asp Thr Ala Gln Ser Thr Ser Arg Gly
 65 70 75

(2) INFORMATION FOR SEQ ID NO:414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Ser Arg Leu Arg Phe Ile Pro Lys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:415:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

Arg Pro Ile Val Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:416:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

Leu Asn Tyr Glu
1

(2) INFORMATION FOR SEQ ID NO:417:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 535 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

AGAGCACCGT CTGCGTGAGG AGATCCTGGC CAAGTTCCTG CACTGGCTGA TGAGTGTGTA	60
CGTCGTCGAG CTGCTCAGGT CTTTCTTTTA TGTCACGGAG ACCACGTTTC AAAAGAACAG	120
GCTCTTTTTC TACCGGAAGA GTGTCTGGAG CAAGTTGCAA AGCATTGGAA TCAGACAGCA	180
CTTGAAGAGG GTGCAGCTGC GGGAGCTGTC GGAAGCAGAG GTCAGGCAGC ATCGGGAAGC	240
CAGGCCCCGCC CTGCTGACGT CCAGACTCCG CTTTCATCCCC AAGCCTGACG GGCTGCGGCC	300
GATTGTGAAC ATGGACTACG TCGTGGGAGC CAGAACGTTT CGCAGAGAAA AGAGGGCCGA	360
GCGTCTCACC TCGAGGGTGA AGGCACTGTT CAGCGTGCTC AACTACGAGC GGGCGCGGCG	420
CCCCGGCCTC CTGGGCGCCT CTGTGCTGGG CCTGGACGAT ATCCACAGGG CCTGGCGCAC	480
CTTCGTGCTG CGTGTGCGGG CCCAGGACCC GCCGCCTGAG CTGTACTTTG TCAAG	535

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 550 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

AGAGCACCGT CTGCGTGAGG AGATCCTGGC CAAGTTCCTG CACTGGCTGA TGAGTGTGTA	60
CGTCGTCGAG CTGCTCAGGT CTTTCTTTTA TGTCACGGAG ACCACGTTTC AAAAGAACAG	120
GCTCTTTTTC TACCGGAAGA GTGTCTGGAG CAAGTTGCAA AGCATTGGAA TCAGACAGCA	180
CTTGAAGAGG GTGCAGCTGC GGGAGCTGTC GGAAGCAGAG GTSAGKCAGC ATCNRSARRC	240
MMKGCTAGCM GCCMTGCYNA YSTCSAGACT SCGCTTCATC CCCAAGCCYR ACKGGCTGCG	300
GCCSATTGTG AACATGRRYT AYRKCRTGGG WGCCAGARCK TTSSGCAGAR RRAAGMRGGC	360
CCAGCATTTTC RCCSAGCGTC TCACCTCGAG GGTGAAGRCW CTSTTCAGCR TGCTCAACTA	420
YGAGCSGGCG CGGCRMYYCG RYMTCMWGGG CGCCTCTRTG CTGGGCCTGG ACGATATCCA	480
CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCYCAG RRCMCGYCGM SKGRGSTGTA	540
CTTTGTCAAG	550

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

GAGTCAGCAT CNACAGACAC TGCTAGCAGC CATGCCNATC TCGAGACTGC GCTTCATCCC	60
CAAGCCCAAC TGGCGGCCCA TTGTGAACAT GAGTTATAGC ATGGGTGCCA GAGCTTTGGG	120
CAGAAGGAAG CAGGCCCAGC ATTTACCCA GCGTCTCAAG ACTCTCTTCA GCATGCTCAA	180
CTATGAGCCG GAATTCGATA TCAAGCTTAT CGATACCGCT CAGAGCACGT CGAGGGGGG	239

(2) INFORMATION FOR SEQ ID NO:420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	Tyr
1				5				10						15	
Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	Lys
			20					25					30		
Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile					
			35					40							

(2) INFORMATION FOR SEQ ID NO:421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

Glu	Ala	Glu	Val	Arg
1			5	

(2) INFORMATION FOR SEQ ID NO:422:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

Ser	Arg	Leu	Arg	Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO:423:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

Pro	Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	Thr
1				5				10						15	

Ile

(2) INFORMATION FOR SEQ ID NO:424:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu
1				5				10						15	

Leu Cys Ser Leu Cys Tyr

20

(2) INFORMATION FOR SEQ ID NO:425:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:426:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:427:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:428:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr
1 5 10 15

Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys
 20 25 30
 Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile
 35 40

(2) INFORMATION FOR SEQ ID NO:429:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

Glu Asn Asn Val Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:430:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg Leu Ile Thr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:431:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg
 1 5 10 15
 Ile

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

```

Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser Ser Phe
1           5           10           15
Leu Cys His Phe Tyr Met
                20

```

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

```

Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr
1           5           10

```

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

```

Gly Phe Glu Lys His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile
1           5           10           15

```

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
1 5 10 15
Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
20 25 30
Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile
35 40

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

Glu Lys Glu Val Glu
1 5

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser
1 5 10 15
Val

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile
1 5 10 15
Leu Ser Ser Phe Tyr Tyr
20

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:442:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

Val	Ser	Arg	Glu	Asn	Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu	Gln	Thr
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:443:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

Trp	Ile	Gly	Ile	Ser	Ile	Asp	Met	Lys	Thr	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO:444:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

Trp	Leu	Phe	Arg	Gln	Leu	Ile	Pro	Lys	Ile	Ile	Gln	Thr	Phe	Phe	Tyr
1				5					10					15	

Cys	Thr	Glu	Ile	Ser	Ser	Thr	Val	Thr	Ile	Val	Tyr	Phe	Arg	His	Asp
			20					25					30		

Thr	Trp	Asn	Lys	Leu	Ile	Thr	Pro	Phe	Ile
		35						40	

(2) INFORMATION FOR SEQ ID NO:445:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

Glu Asn Asn Val Cys
1 5

(2) INFORMATION FOR SEQ ID NO:446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

Phe Arg Ile Ile Ala
1 5

(2) INFORMATION FOR SEQ ID NO:448:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser
 1 5 10 15
 Ile

(2) INFORMATION FOR SEQ ID NO:449:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro
 1 5 10 15
 Ile Val Asp Leu Val Tyr
 20

(2) INFORMATION FOR SEQ ID NO:450:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO:451:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:452:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

Trp	Lys	His	Ser	Ser	Thr	Met	Asn	Asn	Phe	His
1				5					10	

(2) INFORMATION FOR SEQ ID NO:453:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

Ile	Pro	Lys	Lys
1			

(2) INFORMATION FOR SEQ ID NO:454:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

Leu	Leu	Leu	Arg	Leu
1			5	

(2) INFORMATION FOR SEQ ID NO:455:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

Asp Asp Phe Leu
1

(2) INFORMATION FOR SEQ ID NO:456:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GGYTTNGGDA TRAANC

16

(2) INFORMATION FOR SEQ ID NO:457:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

GCNTAYGAYA CNAT

14

(2) INFORMATION FOR SEQ ID NO:458:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

TANGTRTCRT ANG

14

(2) INFORMATION FOR SEQ ID NO:459:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

GGNATHCCNC ARGG

14

(2) INFORMATION FOR SEQ ID NO:460:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

SWNCCYTGNG GDATNCC

17

(2) INFORMATION FOR SEQ ID NO:461:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

YTNGTNGAYG AYTTYT

17

(2) INFORMATION FOR SEQ ID NO:462:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

GTNACNARNA RRAARTCRTC

20

(2) INFORMATION FOR SEQ ID NO:463:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

Asp Asp Phe Leu Leu Val Thr
1 5

(2) INFORMATION FOR SEQ ID NO:464:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,

Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

[illegible]

Xaa Xaa Xaa Xaa Xaa Xaa Gln Gly Xaa Xaa Xaa Ser Xaa
1 5 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

[illegible][illegible]

Phe, Trp or Met, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Tyr or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Asp	Xaa	Xaa	Xaa
1				5					10

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Lys or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

Gly Xaa Xaa Xaa Xaa Xaa Xaa Lys
1 5

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Cys, Lys or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Ser or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Arg or Gln"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Thr, Lys, Tyr or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Glu, Lys or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Cys or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Asp or Phe"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 12
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ser or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 13
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Thr or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Met, Phe or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 6
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ile or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 7
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Glu or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 9
(D) OTHER INFORMATION: /product= "OTHER"

/note= "Xaa = Cys or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ser or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Ile or Val"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

Phe	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Xaa	Tyr	Asp	Xaa	Xaa
1				5					10			

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 30
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 38
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 41
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

```

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1           5           10           15

Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa
20           25           30

Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Xaa
35           40           45

```

(2) INFORMATION FOR SEQ ID NO:472:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 6
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 8
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Ile	Pro	Lys	Lys
1				5						10	

(2) INFORMATION FOR SEQ ID NO:473:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

Xaa Arg Xaa Xaa Pro Lys
1 5

(2) INFORMATION FOR SEQ ID NO:474:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

Xaa Arg Xaa Ile Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:475:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 6

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 8

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 10

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

Pro	Xaa	Leu	Tyr	Phe	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Cys	Tyr	Asp	Xaa
1				5				10						15	

Ile

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 10

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
selected from Ala, Leu, Ile, Val, Pro,
Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

Leu	Leu	Arg	Leu	Xaa	Asp	Asp	Xaa	Leu	Xaa	Ile	Thr
1				5				10			

(2) INFORMATION FOR SEQ ID NO:477:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = any amino acid"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = any amino acid"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = any amino acid"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = any amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

Arg Lys Xaa Xaa Trp Xaa Xaa Leu
1 5